Genetic influences on predicted methane production and natural resource allocation of beef cattle in the Great Plains

by

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Abstract

The environmental impact of the beef industry has recently become an area of increasing scientific investigation. One of the objectives of this thesis was to examine how genetic selection and breeding could influence the environmental sustainability of the beef sector by estimating genetic variance parameters and discovering loci associated with predicted methane traits. Observed feed intake of 830 crossbred steers was used to calculate predicted methane traits via three enteric methane estimation equations from Ellis et al. (2007), Mills et al. (2001), and IPCC (2019). Variance components were estimated using genomic best linear unbiased prediction (GBLUP). Heritabilities for each predicted methane trait ranged from 0.70 to 0.74. Spearman correlations of estimated breeding values for each trait were 0.99. Together, these results suggest any of the three predicted methane, if used for selection, would rank animals very similarly in addition to making genetic progress in a relatively short amount of time. A genome-wide association study was also performed for each predicted methane trait. While none of the single nucleotide polymorphisms (SNP) reached the set significance threshold, an analysis of the 25 SNP nearest to the threshold showed each predicted methane trait was associated with the same genetic loci. Candidate genes found near the top 25 SNP indicate collagen related genes could be tied to predicted methane traits.

Another objective of this thesis was to use a stochastic model to simulate a 100 head cow-calf operation to determine land, water, and fertilizer requirements as well as methane emissions for various regional beef production scenarios. The simulations were parameterized to replicate 74 different land regions in the Great Plains and six varying genetic potentials for mature body weight and peak lactation for cattle within those regions for a total of 444 unique scenarios. Further, the resource inputs of diets including corn products were compared to diets

including grain sorghum products in regions where grains are often fed by cow-calf producers. Lastly, total herd weaning weights for each scenario were estimated based on differences in mature body weight and lactation potential. These weaning weights were used to evaluate resource use efficiency of each genetic potential. The average amount of land use for each herd was 711 hectares when corn products were used and 714 hectares when sorghum products were used. Corn-based diets required an average of 30,588,948 liters of total (irrigation and drinking) water per herd per year, while sorghum-based diets required an average of 42,776,720 liters per herd per year. There were negligible differences in fertilizer estimates between corn and sorghum-based diets (26,532 and 26,523 kilograms of nitrogen per year, respectively). The average enteric methane production for all scenarios was 8,898 and 8,925 kilograms per herd per year for corn and sorghum-based diets, respectively. In general, large, high lactation cattle had the largest environmental footprint, whereas small, low lactation cattle had the slightest. Depending on the variable evaluated, the impact of body size and lactation potential varied in importance. However, animals with a higher lactation potential required more land to grow feedstuffs regardless of size. Although heavier animals had a larger environmental impact than lighter animals with the same lactation potential for total land, blue water, fertilizer, and enteric methane production. When resource use was scaled by kilograms of weaning weight, small, high lactation animals tended to be the most efficient, provided adequate resources can be provided in a cost-effective manner to achieve their genetic potential.

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Chapter 1 - Literature Review of Methane Production Genetics in Beef Cattle

Introduction

Methane (CH_4) is a greenhouse gas (GHG) with 84 times more global warming potential than carbon dioxide (CO_2) over a twenty-year timeframe (Myhre et al., 2013). Domesticated ruminants, which produce CH_4 during their digestive process, are a source of anthropogenic GHGs and contribute to climate change. Gerber et al. (2013) reported domesticated ruminants are responsible for 14.5% of global anthropogenic GHG emissions. More specifically, cattle in both the beef and dairy sectors are responsible for 65% of that 14.5% figure (Gerber et al., 2013). Different areas of the world contribute proportionally more or less to the global emission of enteric methane. For example, Latin America and the Caribbean outstrip the rest of the world in terms of gross emissions related to all beef cattle while South Asia is the greatest source of methane emissions from dairy cattle. (Gerber et al., 2013). The methane produced from ruminant digestion was the largest source of anthropogenic CH_4, contributing 28% of all methane sources in the United States (EPA, 2021). Moreover, enteric fermentation accounts for almost 29% of the total carbon footprint of the agricultural sector (EPA, 2021). Holistically, livestock are responsible for roughly 2-3% of total anthropogenic GHGs in the United States (EPA, 2021).

Even though enteric methane emissions have gotten attention due to their contribution to climate change, it is often overlooked that methane production is a loss of energy and an overall inefficiency in the ruminant digestive system (Johnson and Johnson, 1995). Reducing methane production would not only reduce GHGs but could make animals more profitable.

In order to reduce methane production, thereby slowing climate change and increasing producer profitability, an efficient way of measuring methane on a large scale needs to be found.

This can be done using methane production models, mathematical expressions of enteric fermentation. These are inexpensive, quick, easy, and acceptably accurate (Kebreab et al., 2016). Once a benchmark has been established, next step is to investigate ways methane emissions can be lowered. One avenue available to reduce cattle's carbon footprint is to take advantage of the natural variation between animals and breed specifically for individuals that produce less methane. However, methane production is strongly linked to dry matter intake, which in turn, is strongly linked to economically important traits like body weight and carcass characteristics. Thus, any decisions about reducing CH_4 output from the animal must be weighed against potential losses in productivity or system-wide efficiency. While reducing climate change is vital, it is also imperative that other aspects of sustainability be considered, including consumer needs and producer profitability.

Rumen Function and Methane

Ruminant animals can be considered up-cyclers. They take organic matter that is inedible or lowly digestible in humans, e.g., grass, and transform it into higher quality products, e.g., beef and milk. They are able to do this because of their unique digestive system, which encompasses four compartments. Of those four compartments, the largest in adult animals is the rumen. The rumen is where enteric fermentation takes place. Microorganisms live within the rumen and ferment plant matter by breaking it down on a chemical level. A subset of the microbial population in the rumen are methanogenic archaea which utilize hydrogen and carbon dioxide, waste products of the chemical reactions of the bacteria that directly digest plant matter, to produce methane (Moss et al., 2000). The methane and excess carbon dioxide are eructated or released through the mouth.

When plant matter is digested, it is broken down into hexose. Hexose breaks down into two pyruvate molecules. From pyruvate, the volatile fatty acids acetate, butyrate, and propionate are synthesized. Acetate and butyrate production release hydrogen and carbon dioxide into the rumen. Propionate production releases CO_2 but removes hydrogen from the rumen (Figure 1.1; Ungerfeld, 2013).

Because the hydrogen and carbon dioxide necessary to create enteric methane are products of the rumination process, it follows the more rumination that occurs, the more hydrogen and carbon dioxide are produced in the rumen. The more of those elements that are present, the more substrate methanogenic microorganisms have to feed on, and the more CH_4 they generate (Moss et al., 2000). This central idea plays into three factors that affect methane production: feed intake level, passage rate, and dietary composition.

Total methane production increases as dry matter intake (DMI) increases (Blaxter and Clapperton, 1965; Johnson and Johnson, 1995). In other words, as the amount of feed increases, the more substrates the rumen microbes have to turn into methane.

Passage rate, how quickly feed flows through the rumen into the next digestive compartment, is also an important component in ruminant digestion. In ruminant digestion, the faster the passage rate, the less opportunity there is for microbial action in the rumen; the less microbial action upon feedstuffs, the less methane byproduct is produced. (Moss et al., 2000).

Another major aspect in methane production is dietary composition. Johnson and Johnson (1995) reported the digestion of cell wall fibers increased methane production because of the increased production of acetate. Acetate formation from pyruvate creates hydrogen as a by-product (Moss et al., 2000). It appears the rumen favors acetate formation until the diet reaches 90% concentrate (Johnson and Johnson, 1995), at which point it begins to generate propionate at

higher levels and starch-fermenting bacteria compete with the methanogenic archaea for hydrogen (Moss et al., 2000). Dietary fat also plays a role in enteric fermentation. Fat has been shown to lower methane production, but the exact mechanism remains unknown (Patra, 2013). Hypotheses include lipids lowering feed intake (Kebreab et al., 2016), the rumen prioritizing the biohydrogenation of fatty acids above methane production (Johnson and Johnson, 1995), and inhibited archaea function (Johnson and Johnson, 1995). In summation, the rumen is an intricate ecosystem with many interacting organisms, however knowledge of its function enables prediction of methane production.

Methane Measurement Techniques

In order to reduce the cattle industry's carbon footprint, it is necessary to accurately calculate how much methane cattle are producing during their life. Directly measuring an animal's methane production can be difficult and/or costly. Nonetheless, several techniques have been devised to balance obtaining the highest-quality data with ease and affordability.

Respiration chambers are considered the gold standard of methane measurement because they capture all methane emissions the animal produces while inside. These chambers house animals inside a containment unit attached to a ventilation system. Air is drawn in and out of these vents via a pump system. In-going and out-going air are run through sensors which measure the concentration of CH_4. The difference between the two samples is how much methane the animal produced (Hegarty et al., 2012).

While respiration chambers are the most accurate, respiration chambers do have drawbacks. Chiefly, animals in respiration chambers are stressed due to the unfamiliar conditions and limited space. This stress manifests itself as reduced feed intake, which in turn, reduces methane emissions (Ellis et al., 2007). Moreover, because the animal is confined, it cannot graze

and must be delivered feed. Because animals are not consuming as much and are not fed fresh forages, it is difficult to extrapolate respiration chamber data to pasture animals (Johnson et al., 1994). The cost of constructing the facilities necessary for respiration chambers causes this method of methane measurement to be the most expensive.

A similar, but less intensive form of respiration chambers has been developed for use in feedlots, the milking parlor, or on pasture. These are commonly known as hood calorimeters, headboxes, or under the commercial name of GreenFeed Emission (GEM) units (C-lock Inc., Rapid City, SD, USA). These units offer feed pellets to attract the animal and only measure methane while the animal is visiting the unit. Headboxes work by means of a fan pulling air in past the animal's head, capturing the animal's eructated methane along the way. Hristov et al. (2015) suggested the GEM unit (C-lock Inc., Rapid City, SD, USA) provides an acceptable estimation on methane production, but detailed some potential pitfalls of the technique, such as the process being voluntary and subject to complete head insertion.

Another commonly used methane measurement procedure is the tracer gas technique. An identifiable compound, often sulfur hexafluoride, is in liquid form when it is put inside a tube that allows the compound to escape as a gas at a known rate (Johnson et al., 1994). This tube is inserted into an animal's rumen where the tracer gas is assumed to be emitted in the same quantity as methane (Johnson et al., 1994). By means of a collection apparatus around the animal's mouth and nostrils, the animal's eructation can be captured in a canister carried by the animal. Upon analysis, the quantity of tracer gas can be determined via gas chromatograph, and with it, the quantity of methane (Johnson et al., 1994). Tracer gas is cheaper and less of an imposition on the animal than respiration chambers, however the stress of carrying the collection apparatus and frequent handling to change gas canisters can reduce animal intake and methane

production (Hegarty et al., 2007). Nonetheless, the tracer gas methods produced results very similar to those found in respiration chambers. Grainger et al. (2007) found a slight decrease, roughly 8%, in methane quantity from the respiration chamber to the tracer gas technique and concluded that difference was likely due to the tracer gas method not capturing hindgut methane.

Modeling Methane Production

Directly measuring a group of livestock's methane production can be a drain on both time and funds. Therefore, a variety of methane prediction models have been created. An animal's methane production can be estimated relatively simply and inexpensively when a few variables are input into a model. Models can be either empirical or mechanistic, each with its own advantages and limitations.

Empirical Models

Empirical, or statistical, models are equations used to estimate enteric methane production based on dietary factors (Kebreab et al., 2016). There are a variety of statistical models ranging from fixed values set by the International Panel on Climate Change (IPCC, 2019) to multifaceted equations including linear and nonlinear regressions (Mills et al., 2003). Table 1.1 outlines a few models to illustrate the variety of complexity and options available. Empirical models rely on nutrient intake quantities to estimate the methane output. Generally, either dry matter intake (DMI), gross energy intake (GEI), or metabolizable energy intake (MEI) is used as the basis for most equations, given the fact these measurements are highly correlated with methane production (Blaxter and Clapperton, 1965) and explain the most variation (r^2) between animals (Ellis et al., 2007; Mills et al., 2003).

More variables can lead to better model fit at the expense of increased complexity (Ellis et al., 2007). However, whether the additional effort is warranted appears to be based on the

variation of the diets in the dataset. Ellis et al. (2007), found increased complexity only marginally improved equation accuracy in a dairy dataset where the diets were all very similar. Alternatively, adding more variables greatly improved model accuracy in a beef dataset where different ration compositions had been pooled together because the additional variables accounted for more of the variation found in the beef diets. These variables can range from basic composition of the ration (forage percentage) to more detailed elements (cellulose and fiber content). While quantity of feed is usually the main indicator of methane production, feed composition can play an important role in accurately estimating CH_4. In fact, the equation from Moe and Tyrell (1979) relies solely on measurements of the ration rather than measurements taken from animals, and still is comparable with contemporary models (Ellis et al., 2009).

The primary advantages of empirical models are their relative simplicity, speed, ease of use, and low cost. These models were developed specifically to obtain methane production information without having to measure CH_4 directly, which is both expensive and time consuming. The input variables for empirical models are measurements that are either commonly taken in a research setting (e.g., DMI), determined with proximate analysis of a ration (e.g., cellulose), or estimated from generalized values when ration composition is known but samples of the ration are not available (e.g., gross energy intake (GEI)). Furthermore, empirical models are ideal tools for estimating the methane production of a large population of animals, because of their ability to estimate group means. As an example of empirical models' uncomplicated nature, IPCC Tier 1 (IPCC, 2019) has an established value for the methane output of an individual animal. Alternatively, the next level of complexity, IPCC Tier 2 (IPCC, 2019), has only one variable (GEI).

The key limitation of empirical models is their inherent imprecision. Because they cannot capture every facet of methanogenesis these models cannot be perfectly accurate. Escobar-Bahamondes et al. (2016) performed an evaluation of 54 extant equations using datasets from beef cattle fed high-forage and low-forage diets. The authors found the best fitting equations for the high-forage diets had root square mean prediction error (RSMPE) of 23.9 to 28.6%, where lower values indicate greater accuracy. Similarly, the best fit equations had concordance correlation coefficients (CCC) ranging from 0.601 to 0.725, where positive one indicates perfect concordance. The equations for the low-forage dataset were less precise with RMPSE ranging from 32.3% to 57.3% and CCC of 0.354 to 0.521. Ellis et al. (2010) performed a similar evaluation on nine equations with both group means and individual information on dairy cattle. This study showed RMSPE of 24.0% to 38.2% and CCC of 0.000 to 0.271 for the group mean dataset. Alternatively, the individual dataset had RMSPE of 20.2% to 52.5% and CCC of 0.009 to 0.493. Holistically, while empirical models do provide a reasonable estimate of methane production, they are not perfectly accurate and any estimates should be reported with an estimate of error.

The same simplicity that is a boon to empirical models can also be a drawback. Because these models rely on relationships between nutrient intake and methane emissions without accounting for any underlying biology, the models may produce results that go against known biological principles (Ellis et al., 2010; Johnson and Johnson, 1995). Dietary fat, for instance, increases energy intake, but lowers methane production. A meta-analysis performed by Patra (2013) on 29 experiments totaling 1339 observations showed fat supplementation decreased CH_4 output. In this particular example, using models involving factors like GEI and MEI without a dietary fat component would lead to an overestimation of methane production. Because

empirical models can only account for the variables they are given, all other factors are considered random error when the models are evaluated. Because the rumen is a complex and ever-changing environment with relationships and mechanisms that are still unknown, it is impossible to create a simple, easy-to-use equation that captures and quantifies every variable.

Moreover, empirical models tend to fail when they are used outside of the specific scenario for which they were developed. For example, if a model developed based on information from dairy cattle is applied to a feedlot dataset, the accuracy is drastically reduced (Moraes et al., 2014). Expanding even further, empirical models bring animals to the average, losing any differences between animals with the same predictor variables. This variation, however, is the key to selection and genetic progress.

Mechanistic Models

Contrary to empirical models, mechanistic models, also known as dynamic models, attempt to emulate the biological process of methanogenesis in the rumen. These models simulate the interaction between microbial populations, feed substrates, and environmental conditions like pH and passage rate to estimate how much hydrogen will be available to reduce CO_2 into CH_4 and water (Bannink et al., 2011). More precisely, mechanistic models attempt to estimate hydrogen sources and sinks with the underlying assumption that all excess hydrogen will be used in CH_4 production. They accomplish this by utilizing various sub-models that work together so the output of one model becomes the input for another.

The first set of inputs in a mechanistic model are centered around feed. Each model has its own specific set of inputs, but all models share a few common ration elements such as protein, ammonia, lipids, starch, cellulose, and hemicellulose expressed as moles, and microbial population pools, expressed as grams (Baldwin, 1995; Dijkstra et al., 1992). While the chemical

composition of the ration is important, there are other feedstuff characteristics required by most mechanistic models, including feed intake and various factors that affect passage rate like particle size (Baldwin, 1995; Dijkstra et al., 1992).

One unique facet of dynamic models is the microbial pools. Microbial pools are the sub-models that change the simulated feed substrates, such as corn, soybean meal, or hay, into the intermediates (monosaccharides, oligosaccharides, and unsaturated fatty acids), which determine how much methane will be produced. Dijkstra et al. (1992) categorized microbes into three populations: amylolytic which digest starch, fibrolytic/cellulolytic which digest structural carbohydrates like cellulose, and protozoa, which are both amylolytic and predatory to fibrolytic cells. The separation of microbial pools allows for the model to be more finely tuned relative to the extent and speed that feedstuffs are digested.

The alternate approach, modeling the microbial pool as a single whole, was developed by Baldwin (1995). This model assumes the difficulty of parameterizing complex microbial interactions outweighs any accuracy the model would gain from doing so. It can be challenging to determine what proportion of small saccharide products are fermented by the amylolytic and cellulolytic populations and in what proportion by the soluble carbohydrate fermenters (Baldwin et al., 1970). Additionally, specifying a set of volatile fatty acid (VFA) stoichiometric coefficients for each pool can lead to inaccuracy because the exact mix of microbes varies heavily with diet (Baldwin, 1995).

One of the most important components of mechanistic models is volatile fatty acid stoichiometry, i.e., the relative concentration of each VFA. The amount of a specific VFA produced can be predicted by the quantity and composition of substrate fermented in the rumen (Argyle and Baldwin, 1988; Bannink et al., 2006; Murphy et al., 1982). Each VFA has a

chemical reaction required to produce it and each reaction has its own set of products and reactants. Often, one of those products is hydrogen. Because hydrogen gas is the limiting reactant for methane production, the amount of hydrogen in the rumen has a direct correlation on the amount of methane emitted. Thus, by determining how much hydrogen is released and used in the formation of VFAs, the quantity of free hydrogen gas can be calculated, which, in turn, corresponds to the volume of methane produced.

As shown in Figure 1.2, the models assume hydrogen is used to: i) support microbial growth with ammonia (0.41 mol H_2/g microbial matter), ii) biohydrogenate unsaturated fatty acids (2 mol H_2/ mol unsaturated fatty acid), iii) produce propionate and valerate (1 mol H_2/ mol VFA), and iv) reduce CO_2 to CH_4 and water (Baldwin, 1995).

Originally, dynamic models only dealt with methane from microbes in the rumen (87-90% of all ruminant methane (Murray et al., 1976)), but an advancement by Mills et al. (2001) made it possible to estimate production of methane from hindgut fermentation. The addition of hindgut methanogenesis enables a more accurate estimate of total animal CH_4 production.

There are two key advantages mechanistic models have over their empirical cousins: improved accuracy and assessment of mitigation options. Because mechanistic models rely on the biology of nutrient digestion and absorption, they are more sensitive to changes in the diet. For example, lipids are generally considered antagonistic to methane production (Kebreab et al., 2016). However, the most accurate empirical models do not account for them while mechanistic models do. The additional sensitivity makes mechanistic models more accurate. Benchaar et al. (1998) showed that mechanistic models explained 70% of the variation between actual methane production observations whereas empirical models only explained 42-57%. The greater accuracy of dynamic models was demonstrated again by Kebreab et al. (2008), where two mechanistic

models more accurately predicted observed methane production than two empirical models. One mechanistic model was better for dairy data while the other was better for feedlot data, but both exceeded the predictive power of the empirical models.

The other advantage of mechanistic models is the ability to assess methane mitigation options. Empirical models are direct relationships between feedstuffs and methane output; therefore, they lack the nuance necessary to assess possible mitigation strategies. Dynamic models can evaluate small adjustments, making them the best tool for the assessment of mitigation practices. According to Kebreab et al. (2006), mechanistic models are the preferred tool when evaluating methane mitigation through dietary changes. Mitigation strategies need to be assessed for total methane production, but also need to be realistic and profitable.

A major drawback of mechanistic models are the intrinsic complexities and numerous inputs required to operate them. Dynamic models rely on VFA stoichiometry to determine how much excess hydrogen will be available for CH_4 production. Therefore, if the estimates of the VFAs are inaccurate, all of the downstream data, including methane production, are inaccurate. Morvay et al. (2011) performed an evaluation of models that predict VFA stoichiometry. Though the best fit model, developed by Bannink et al. (2006), did well when it estimated acetate and propionate it had much higher root mean squared prediction error for butyrate, valerate, and other branched chain VFAs.

Furthermore, mechanistic models are large, possibly requiring up to 19 variables (Bannink et al., 2011) including feed quality measurements which are not commonly taken (e.g., cellulose, hemicellulose, and lignin). Because of this, dynamic models may be deemed too complex for many purposes. Instead, researchers may utilize empirical models and accept the decreased accuracy of predictions for a given dataset (Kebreab, et al., 2006).

There are two commonly used dynamic models used in the literature. The first is MOLLY, developed in its modern form by Baldwin (1995) using the VFA stoichiometry of Murphy et al. (1982). MOLLY adapts the equations of Argyle and Baldwin (1988) to account for the effects of water kinetics and pH on rumen stoichiometry. MOLLY has 15 input variables and one microbial pool. The other frequently used dynamic model is known as COWPOLL. It was originally developed by Dijkstra et al. (1992), then updated to include intestinal fermentation (Mills et al., 2001), along with a revised VFA stoichiometry sub-model by Bannink et al. (2008). Though COWPOLL was developed for dairy cattle modeling (and performed very well in Kebreab et al. (2008), with a CCC of 0.75 for dairy cattle), it was modified for beef cattle by Ellis et al. (2010). Moreover, COWPOLL was adapted by Bannink (2011) to be utilized as the IPCC Tier 3 methane prediction model. When the two mechanistic models were compared, MOLLY outperformed COWPOLL in predicting methane output from feedlot cattle (Kebreab et al., 2008).

Conclusion

Methane models are a relatively quick and simple way to estimate how much methane a ruminant will produce. The simpler equations like the IPCC Tier 2 model (IPCC, 2019), provide a rough estimate that is best for assessing the amount of methane a given population of cattle is producing at the moment. More complex models, such as the mechanistic models, require more information than the empirical models, but provide greater accuracy and allow for the investigation of mitigation options.

Heritability of Methane Production

One possibility to reduce enteric methane production that has been considered by the scientific community is to breed animals that naturally produce less methane. For this strategy to

be effective, methane production must be a heritable trait. Further, in order to approximate how quickly progress can made, it is useful to know how much variation in a population is genetic. Methane production heritabilities have been estimated in a variety of populations. Thus, a wide range of heritability estimates for methane production exists in the literature.

In cattle, heritability estimates have been taken on different populations with different measurement techniques, such as beef or dairy animals with methane production measured either directly or predicted with equations. Thus, heritability estimates in the literature have ranged from 0.07 to 0.52.

Fortunately, Brito et al. (2018) performed a meta-analysis of 60 published articles looking at an assortment of methane-related traits in both cattle and sheep. The authors used the reported standard error (estimated in cases where no standard error was reported) in order to weight each estimate in the analysis. Then the authors fit a random-effects model where the published estimate from each study was equal to the weighted population parameter mean, plus the among-study deviation from the mean, plus residual error.

Four meta-analysis scenarios were studied: one looking at cattle and sheep data together, one with just cattle data (Table 1.2), one with just sheep data, and one using only cattle data comparing studies that used direct observation to studies that used predictions. Heterogeneity was calculated along with a 95% confidence interval for each methane related trait in each scenario. When looking solely at methane production for only cattle data, Brito et al. (2018) found the average heritability estimate was 0.25 ± 0.02. The 95% CI was calculated to be (0.22 - 0.29). Though the standard error was fairly low, the estimates in the literature varied greatly. The root cause of the inconsistences seems to be coming from articles that utilized predicted methane emissions rather than direct measurements in order to estimate heritability. When breaking

publications down into studies that used direct methane measurements and those that used predicted values, studies in the former group showed no significant variation. Conversely, the estimates of studies which employed predicted methane measurements exhibited large amounts of variation. This variation is most likely based in the fact that prediction models are simply estimates of methane production, not actual observations. In other words, there is some embedded uncertainty in those phenotypes. Further compounding the issue, is heritability is also an estimate with its own uncertainty and error. It is logical for the heritability estimates of methane production based on prediction equations to have high variation because the heritabilities are estimates of estimates.

Conclusion

Methane is a low-to-moderately heritable trait. Therefore, it is possible to reduce methane through selection and breeding and to estimate the rate at which genetic progress can be made. However, genetic progress through selection can only be made if methane production phenotypes are collected on large numbers of candidates for selection. These phenotypes would also need to be direct measures of methane production because while predicted methane equations are good tools when a gross accounting of methane production is needed, they fail when it comes to providing the fine level of variation between individuals required for selection. If methane production based on prediction equations were used for selection, methane production would not be the only trait affected because methane production is highly correlated with other economically important traits.

Methane and Relationships to Other Traits

When selecting on a trait, such as methane production, it is important to know the other traits with which the trait of interest has correlations. In other words, it is important to know how

the performance of other traits will be affected before selection begins. In beef production, economically important traits that may be related to methane include growth, feed efficiency, and meat quality.

Dry Matter Intake

The relationship between dry matter intake (DMI) and methane production in ruminants has been known at least since the first half of the 20th century. The relationship between the two traits is strongly positive. If dry matter intake increases, methane production also increases. This is because the more an animal ingests, the more substrates there are for the rumen microbiome to break down. A byproduct of this microbial degradation is hydrogen which, along with carbon dioxide, is reduced by methanogenic archaea to produce methane gas (Hungate, 1967). Further, a diet of roughages has been shown to increase methane production compared to a diet of primarily concentrates (Johnson and Johnson, 1995).

A study authored by Kriss in 1930 was one of the first papers examine the correlation between DMI and methane production. The author analyzed a series of 131 respiratory calorimetric experiments, 123 with steers and 8 with dry cows. Of these trials, 54 offered the subjects roughage rations while the other 77 trials offered a mix of roughage and grain. Kriss (1930) found the phenotypic correlation between the DMI of the animals and the methane production to be 0.942 (0.01) for roughage diets and 0.963 (0.006) for the mixed diets. Compared to later estimates, the correlations reported by Kriss (1930) are rather high, possibly because of the state of technology used to measure methane available when this study was conducted. Alternatively, it may be because Kriss (1930) combined data from steers of various weights with mature cows which resulted in the kind of statistical variation that was not possible to account for with the methodology of the time.

Nkrumah et al. (2006) selected 27 feedlot steers for differences in residual feed intake (RFI) in order to determine the associations between RFI and other traits. In the process, the authors measured methane production in an indirect calorimetry system and DMI was measured via an automated feeding system. Nkrumah et al. (2006) estimated the phenotypic correlation between methane production and DMI to be 0.38 ($P < 0.05$). Contrary to Kriss (1930), the estimates of Nkrumah et al. (2006) are fairly low. This might be because the study only consisted of 27 animals or because the animals were selected for differing residual feed intake which, as noted in a later section, may influence the amount of methane an animal produces.

Similarly, Fitzsimons et al. (2013) performed an experiment evaluating the relationship of RFI with other traits. Fitzsimons et al. (2013) analyzed the methane production of 22 Simmental heifers on a grass silage diet using the sulfur hexafluoride (SF_6) tracer gas technique developed by Johnson et al. (1994). Fitzsimons et al. (2013) measured each animal for five consecutive days during two periods. The authors found the phenotypic correlation of methane production and DMI to be 0.43 ($P < 0.01$).

Herd et al. (2014), Manzanilla-Pech et al. (2016), and Donoghue et al. (2016) all reported very similar phenotypic correlations between DMI and methane production. These three studies produced phenotypic correlations between methane production and dry matter intake of 0.65 (0.02), 0.70 (0.02), 0.71 (0.02), respectively. The similarity in the three figures may be because Manzanilla-Pech et al. (2016) and Donoghue et al. (2016) are extensions of Herd et al. (2014). The 777 Angus bulls and heifers used in Herd et al. (2014) made up a large portion of the 1020 and 1046 Angus animals used in Manzanilla-Pech et al. (2016) and Donoghue et al. (2016), respectively. These studies were able to utilize a comparably large number of animals by taking advantage of federally owned cattle herds and measuring the animals over the course of multiple

years. The protocol required the animals to be trained in a respiration chamber for a 24-hour period then measured for methane production in a different chamber for two consecutive 24 hours periods. The large difference between the estimates from Nkrumah et al. (2006) and Fitzsimons et al. (2013) and these three studies is unclear but may be because the latter studies had a much larger sample size or because the animals were not selected based on differences in residual feed intake.

Herd et al. (2016) performed three trials in an attempt to evaluate the phenotypic relationship between methane production and feed efficiency. The first was performed in a feedlot setting, allowing the animals to eat ad libitum (n = 41). The other two were done in respiration chambers wherein one group was limit-fed grain (n = 59) and the other limit-fed forage (n = 57). For the feedlot trial the authors utilized two GreenFeed Emission Monitor (GEM) units (C-lock Inc., Rapid City, SD, USA). The relationship between DMI and methane production varied across all three, with correlations of 0.28 ($P < 0.10$), 0.55 ($P < 0.05$), and 0.61 ($P < 0.05$), for the feedlot trial, grain-fed chamber trial, and roughage-fed chamber trial, respectively. The association between methane production and DMI for the respiration trials is lower than reported by Herd et al. (2014), Manzanilla-Pech et al. (2016), and Donoghue (2016). However, the feedlot trial produced a surprisingly low correlation, even lower than Nkrumah et al. (2006), which may be due to how the methane measurements were collected.

In another paper examining the differences between high and low RFI animals, McDonnell et al. (2016) found methane production phenotypically correlated with DMI at 0.42 ($P < 0.05$), but only when animals were on pasture. In this study, 28 Limousin-Friesian cross heifers, 14 with high phenotypic RFI and 14 with low phenotypic RFI, were monitored over three periods. The first period lasted 40 days and the animals were fed grass silage. The next

period last 57 days and the animals were turned out onto a perennial ryegrass pasture. The final period lasted 41 days and the heifers were supplied with a mixed ration of 70% concentrate and 30% corn silage. Dry matter intake was measured as the difference between feed offered and feed refused for Period 1, the *n*-alkane technique developed by Mayes et al. (1986) for Period 2, and an automated feed intake system for Period 3. Methane production was measured for 5 days during each period using the SF_6 technique (Johnson et al., 1994). When methane production was correlated with DMI within each period, the only significant phenotypic correlation was found when the animals were on pasture. The authors acknowledged DMI is generally highly correlated with methane production in ruminants; however, they noted the only significant correlation between the two traits was found when the technique for calculating DMI was most error prone. Moreover, the authors also admit that due to the nature of the experiment, the diet period was inextricably confounded with age and body weight, both of which influence DMI and methane production.

Velazco et al. (2016) performed a very similar experiment as McDonnel et al. (2016). The authors observed the actual methane production of 39 Angus cattle that differed in RFI while the animals were on pasture. The cattle in Velazco et al. (2016) were separated into two groups; one group was comprised of 19 steers and the other had 20 heifers. To measure individual methane production, the authors set up two GEM (C-lock Inc., Rapid City, SD, USA) units in the paddocks where each group was grazing. The animals were rotated between paddocks to avoid confounding sex, paddock, and monitoring unit. Additionally, the authors used the equation of Minson and McDonald (1987) to predict DMI on pasture. This equation uses liveweight and average daily gain to estimate dry matter intake within 1% of the actual DMI, as reported by the equation's original authors (Minson and McDonald, 1987). When the

authors ran Pearson correlations between methane production and predicted DMI, the result was 0.41 ($P < 0.05$). Not surprisingly, the correlation between methane production and dry matter intake calculated by Velazco et al. (2016) is similar to that calculated by McDonnel et al. (2016).

In an Australian study, Bird-Gardiner et al. (2017) analyzed two datasets separately but with the same methodology. One set was 119 Angus heifers (interestingly, these were the progeny of the animals used in Donoghue et al. (2016)) who were feed an *ad libitum* diet of alfalfa and oaten hay chaff. Several cohorts of Angus steers, 326 in total, made up the other dataset. The steers were fed a high-grain feedlot diet. Both sets of animals had methane production measured by GEM (C-lock Inc., Rapid City, SD, USA) units; the heifers for a 15-day period and the steers for 70 days. The correlation between methane production and DMI found by Bird-Gardiner et al. (2017) are in line with those published by Herd et al. (2014), Manzanilla-Pech et al. (2016), Donoghue et al. (2016), and Herd et al. (2016). The correlations between the two traits for the heifers was 0.75 ($P < 0.05$), while the correlation for the steers was 0.62 ($P < 0.05$). The authors hypothesize the correlation was greater for the heifers because those animals' diet rather than sex or location, although the factors were confounded.

Renand et al. (2019) also investigated the methane production of heifers fed an *ad libitum* roughage diet. This study focused on 22-month-old Charolais heifers. Of the total 326 heifers, 258 were kept as at a farm near Galle, France and the other 75 head were kept at a research farm near Borculo, France. The Galle farm fed the heifers housed there a diet comprised primarily of fescue silage, while the animals at the Borculo facility received meadow hay. Both facilities measured methane production using a GEM (C-lock Inc., Rapid City, SD, USA) unit and calculated DMI as the difference in dry matter between feed offered and feed refused. Although the animals were the same breed and both fed roughage diets, the correlation between methane

production and dry matter intake varied. For the heifers at the Galle farm the correlation was 0.36 ($P < 0.001$). Alternatively, the heifers at the Borculo farm had a correlation of 0.48 ($P < 0.001$). While the correlations between each farm may be different, perhaps owing to the difference in digestibility between silage and hay, neither correlation is too far off from other studies in the Northern hemisphere, including Nkrumah et al. (2006), Fitzsimmons et al. (2013), and McDonnel et al. (2016).

Thus far, the correlations between methane production and DMI which have been discussed are solely phenotypic correlations. While phenotypic correlations are important, they only reflect phenotypes and do not provide insight into the genetic relationships between traits. Genetic correlations, such as those generated by Donoghue et al. (2016) and Manzanilla-Pech et al. (2016), can provide this information.. Donoghue et al. (2016) calculated a genetic correlation between methane production and DMI of 0.84 (0.06) using a traditional best linear unbiased prediction (BLUP) analysis implemented in ASREML software. Manzanilla-Pech et al. (2016) had access to genomic information, allowing the authors to create a genomic relationship matrix and perform a genomic best linear unbiased prediction (GBLUP) which yielded a genetic correlation of 0.83 (0.05).

Live Weight

The previous studies show methane production is moderately to highly correlated with DMI. Dry matter intake is also strongly related to body weight and growth in cattle (Herd et al., 2014; Donoghue et al., 2016; Manzanilla-Pech et al., 2016). Those two facts help explain why methane production is also linked to growth traits and overall body weight.

The weight of an animal is usually taken at several points during its life. In the beef industry, those weights are commonly measured at birth, weaning, one year of age, and as a final live weight or mature weight.

Before discussing the relationships, it should be noted that in Herd et al. (2014), Donoghue et al. (2016) and Manzanilla-Pech et al. (2016), a majority of the animals were approximately one year old (a smaller proportion were approximately two years old) when the methane measurements were taken. Thus, all correlations from those three papers should be interpreted as live weight at various ages correlated with methane measurements when the animal was roughly one year old. As shown in Table 1.3, the phenotypic correlation between methane production and birth weight is relatively low. Herd et al. (2014) reported the association at 0.19 (0.05), while Donoghue et al. (2016) published a correlation of 0.26 (0.04). At weaning, the correlation of live weight with methane production jumps to roughly 0.50 and increases further at yearling to approximately 0.60. However, correlations with finished weight show a modest reduction in the correlation, similar to that exhibited at weaning.

In this case, the genetic correlations between methane production and weight traits are higher than the phenotypic correlations. As Table 1.3 shows, the genetic correlations follow the same curvilinear pattern as the phenotypic correlations (Donoghue et al., 2016).

Manzanilla-Pech et al. (2016) reported slightly different correlations. In the Manzanilla-Pech et al. (2016) study the phenotypic correlation of methane production and test live weight (when the animals were approximately one year old) was 0.67 (0.02) and the genetic correlation between the two traits was 0.80 (0.06).

Angus cattle, the breed used in Herd et al. (2014), Donoghue et al. (2016), and Manzanilla-Pech et al. (2016), were not the only breed to show significant associations between

methane production and liveweight. Renand et al. (2019) examined two populations of 22-month-old Charolais heifers for methane production. When the authors correlated the body weight and methane production for each population, they reported very similar numbers. The Galle herd had a correlation of 0.68 ($P < 0.001$) whereas the Borculo herd had a correlation of 0.70 ($P < 0.001$).

On the whole, live weight is strongly correlated with methane production. This can be explained logically as on average the heavier the animal, the more feed it consumes, and the more feed it consumes, the more methane it produces; alternatively, larger animals may also have larger rumens, larger rumens imply more microbes, which in turn imply more methane production. Therefore, in order to lower methane production and maintain the same weight producers and packers have come to expect, it is important to select more feed efficient animals.

Average Daily Gain and Feed Efficiency

Average daily gain (ADG) estimates how much an animal's body weight increased on a daily basis over a period of time. Because beef animals are usually feed to a certain end weight, animal that reach that goal more quickly may increase profitability. Further, because ADG and feed efficiency are closely tied to cost of gain, measures of feed efficiency are important for the commercial cow-calf, stocker, and feedlot sectors.

Feed efficiency directly affects producers' bottom line by determining the amount of feed required; therefore, it is important to estimate the relationship between feed efficiency and methane production when evaluating methane reduction strategies. This is precisely what Freetly and Brown (2013) did when the authors regressed methane production on the ratio of body weight gain to dry matter intake, known as gross feed efficiency (GFE). Freetly and Brown (2013) had two groups of interest, a group of 37 steers with ad libitum access to a finishing diet

and a group of 46 heifers provided a ration of 60% corn silage, 30% alfalfa hay, and 10% wet distiller's grain. The DMI of each animal was measured for one day, which may have been insufficient for accurate DMI estimates, before the animals were moved into respiration chambers for 15 days to measure their methane production. The animals also had their RFI calculated as the residual errors of a regression of ADG and mid-test metabolic body weight ($BW^{0.75}$). The steer and heifer data were treated as distinct and the regression of methane production on GFE and DMI was performed for each sex. For the steers, neither GFE nor DMI were significant in explaining the variation of methane production. In contrast, both predictor variables provided some information for the heifer data. In particular, GFE had a regression coefficient of 231.9 (standard error of 99.3, $P < 0.02$), indicating that as GFE increased, methane production also increased. Whether this finding was due to sex or diet is impossible to tell.

During the feedlot portion of the trials performed by Herd et al. (2016), the animals were measured for ADG and feed conversion ratio (FCR) which is ratio of DMI and ADG (DMI/ADG). These feed efficiency and growth measurements taken in the feedlot were tested for correlation in the three settings in which methane was gathered: a feedlot, a respiration chamber when the animals were fed grain, and a respiration chamber when the animals were fed roughage. The only significant correlation the authors reported was between feedlot FCR and methane production from the roughage-fed chamber test. The relationship was a negative correlation, -0.31 ($P < 0.05$), implying methane production had an undesirable association with FCR because lower FCR values indicate more efficient animals. Though the lack of significance between FCR and methane production in the other settings does seem to make the significant correlation a tenuous one.

While Herd et al. (2016) did not find a significant correlation between methane production and ADG, Velazco et al. (2016) did. In that study, the authors reported a Pearson correlation coefficient of 0.33 ($P < 0.1$) between daily methane production and ADG. This finding suggests animals that produce more methane also gain more body weight per diem. Unlike Herd et al. (2016), Velazco et al. (2016) did not find a significant correlation between methane production and FCR, though in the case of the latter study FCR was based on predicted DMI estimates, which may not have captured the outliers.

Renand et al. (2019) collected data on several measures of feed efficiency including feed efficiency ratio (FER). A feed efficiency ratio is ADG divided by DMI, the reciprocal of FCR. Renand et al. (2019) found ADG was significantly correlated with methane production at 0.44 ($P < 0.001$) and 0.26 ($P < 0.05$) for the Galle heifer group and Borculo heifer group, respectively. In contrast, only the Galle heifers had significant associations between methane production and FER. This correlation is small at 0.14 ($P < 0.05$). This study also calculated residual ADG, or the difference between observed ADG and expected ADG as determined by regressing ADG on metabolic body weight and DMI. For residual ADG, positive values are more desirable because positive values indicate animals gained more per day than expected. Residual ADG only had a significant small correlation with methane production in the Galle heifers at 0.17 ($P < 0.01$).

The results reported here indicate methane production is positively associated with growth and gain. This makes logical sense because the more animal eats, the more weight it gains and the more methane it produces. Further, it seems feed efficiency is associated with methane production in a manner which indicates the more efficient an animal is, the more methane it will produce. This too makes logical sense because most of the feed efficiency traits discussed thus far have been ratios involving gain and DMI. This begs the question: What is the

connection between methane production and a measure of feed efficiency for which weight and gain have been accounted?

Residual Feed Intake

Residual feed intake is another measure of feed efficiency which has often been investigated alongside methane production. Residual feed intake is the difference between observed feed intake and the expected feed requirements for an animal of a given weight, rate of gain, and body composition. Expected dry matter intake can be calculated by performing regression of DMI on ADG and metabolic body weight (Koch et al., 1963).

Residual feed intake has been phenotypically and genetically linked with methane production in several studies. Nkrumah et al. (2006) followed a group of 29 steers for two years. Steers were separated into three groups: high, medium, and low RFI, as determined by the standard deviations (SD) from the means of their respective contemporary group. The high-RFI cattle had RFI greater than 0.5 standard deviations (SD) above the mean, the medium animals ranged ± 0.5 SD around the mean, and steers ranked as low RFI were 0.5 SD below the mean. The phenotypic relationship between methane production and RFI was calculated as moderate and positive at 0.44 ($P < 0.05$). Furthermore, low RFI steers produced 28% less methane per day than high RFI animals and 24% less than medium RFI animals.

One of the next papers to explore the relationship between methane production and RFI was Hegarty et al. (2007). Three measurements of RFI were defined: RFI_{EBV} which is the midpoint of the parental expected breeding values (EBV) for RFI, RFI_{70d} which is the observed individual RFI for the 70-day testing period, and RFI_{15d} which denotes the residual feed intake for the 15 days the animals were under observation for methane collection. The authors chose to use RFI_{15d} to reflect the diminished feed intake brought on by the stress of using the SF_6

technique (Johnson et al., 1994). The authors of Hegarty et al. (2007) performed a linear regression to predict methane production using RFI_{15d} as the independent variable. The resulting equation indicated reducing RFI_{15d} by 1 kilogram per day would reduce methane production by 13.3 gram per day ($r^2 = 0.12$, $P < 0.01$). This result, while significant, does not explain much variation in the data possibly due to the confounding factors involved in only measuring RFI for 15 days rather than the standard 70 days. Hegarty et al. (2007) also compared the methane production from the ten highest RFI_{15d} steers and the ten lowest RFI_{15d} steers. The low RFI_{15d} animals emitted 25% less methane than the high RFI_{15d} animals, which is consistent with Nkrumah et al. (2006).

Fitzsimons et al. (2013) compared high-RFI heifers to low- and medium-RFI heifers. Each group was measured for total methane production and metabolic methane intensity (defined as methane output adjusted for metabolic body weight). The high-RFI heifers averaged 297 grams of methane per day whereas the low-RFI heifers averaged 260 grams, a significant difference ($P < 0.05$). Likewise, the high RFI-heifers produced significantly more grams of methane per kilogram of metabolic body weight than the low-RFI heifers, 2.9 and 2.5, respectively ($P < 0.05$). Interestingly, VFAs were also measured and the low-RFI group had a higher concentration of propionate ($P < 0.10$) and a lower acetate:propionate ratio than the high-RFI heifers (3.5 vs. 4.6, $P < 0.07$). This suggests more hydrogen is being directed toward propionate production and less excess hydrogen for the formation of methane in lower RFI animals.

Alemu et al. (2017) performed an observational study including RFI and methane production phenotypes. The authors detailed a trial in which 98 crossbred heifers were tested for 72 days to gauge their individual RFI. Of those 98 heifers, 16 were selected for methane testing,

8 with negative RFI and 8 high positive RFI. Both groups had similar body weights and ADG. This subset of heifers was tested for methane production over two 25-day periods. During each period, each animal spent two days in a respiration chamber and the rest of the time in a pen equipped with a GEM (C-lock Inc., Rapid City, SD, USA) unit. When methane production was measured in the open lot, the low-RFI heifers had significantly lower emissions than the high-RFI heifers, averaging 202.5 grams per day and 222.2 grams per day ($P < 0.02$), respectively. In contrast, when methane production from the respiration chamber was compared between groups, there was no significant difference ($P < 0.4$). The authors speculated this is likely because the added stress of being in respiration chamber depressed DMI, which, in turn, brought down methane production. Both groups exhibited a significant decrease in methane production ($P < 0.001$) between the GEM (C-lock Inc., Rapid City, SD, USA) and respiration measurement techniques.

In a Canadian experiment, the authors of Manafiazar et al. (2020a) examined yearling heifers and mature cows for methane production and RFI-fat (RFI with backfat added as predictor variable in the regression equation) under dry lot conditions. This study consisted of eight trials using yearling heifers and six trials using mature cows. In total there were 147 high RFI-fat heifers, 69 high RFI-fat cows, 167 low RFI-fat heifers, and 70 low RFI-fat cows selected for methane production analysis. Each trial was conducted for at least 72 days after an initial adjustment period where the animals had their methane production measured via a GEM (C-lock Inc., Rapid City, SD, USA) unit. Numerically, the low RFI-fat heifers produced less methane than the high RFI-fat heifers and this trend continued in the mature cows. However, inference on the effect of RFI-fat on methane production cannot be made because of a significant statistical interaction between trial and RFI-fat.

Interestingly, heifers from Manafiazar et al. (2020a) were followed into the pasture setting and re-measured for methane production using both a GEM (C-lock Inc., Rapid City, SD, USA) unit and an open path Fourier-transform infrared spectrophotometer (OP-FITR) as detailed in Manafiazar et al. (2020b). The heifers retained the designations of high or low RFI-fat from the previous study; however, each animal had new DMI phenotype which was determined using indigestible pellets recovered by fecal sampling twice daily. Two trial periods were of interest, one lasting seven days while the heifers were being dosed with alkane (adjustment period) and the four days following that period (assessment period). When methane production was being measured by the GEM (C-lock Inc., Rapid City, SD, USA) unit, there was no significant difference in methane production between the high and low RFI-fat groups during the adjustment period. In contrast, during the assessment period when methane production was measured using the GEM (C-lock Inc., Rapid City, SD, USA) unit, the low RFI-fat heifer produced significantly less methane than the high RFI-fat heifers (238.7 grams per day and 250.7 grams per day, respectively, $P < 0.009$). Alternatively, methane production was measured using the OP-FITR, which was only during the assessment period, the low RFI-fat heifers produced numerically less methane; however, there was significant interaction between RFI-fat and testing method, preventing further inference on the main effect of RFI-fat.

Not all studies report a relationship between methane production and RFI, especially on different nutritional planes. Jones et al. (2011) examined two groups of beef cows, one with high EBVs for RFI and the other with low EBVs for RFI. These EBVs were calculated based on each animal's record of a post-weaning RFI test done earlier in the animal's life. Methane emissions were measured by an OP-FITR in each group during two different periods: once while pregnant and consuming a poor-quality forage and again while the cows were lactating and grazing a

high-quality, highly digestible forage. There was no difference in methane production between the two groups while the animals were grazing low-quality pasture. In contrast, while nursing, the low-RFI group exhibited a more favorable methane intensity, or grams of methane per kilogram of body weight, than the high-RFI animals (0.34 vs. 0.46, $P < 0.05$). The authors suggest the poor-quality forage did not have enough crude protein to adequately support the rumen microbial population, thus making the low-RFI animals unable to fulfill their genetic potential.

Freetly and Brown (2013) preformed a multiple regression analysis of methane production on RFI and each animal's 24-hour DMI before the methane measurement on both a group of steers and a group of heifers. The results indicated RFI was not a significant predictor of methane production for either steers or heifers. Therefore, the authors concluded methane production does not decrease with increased feed efficiency.

Mercadante et al. (2015) noted mixed results for the relationship between methane production and RFI. In this study, Nellore cattle were performance tested for RFI and methane production. The animals consisted of a group of 56 heifers and a group of 62 steers, each fed the same ration of 45.5% hay and 55.5% concentrate. Both groups were subjected to what the authors termed an RFI-growth period, consisting of over 100 days for each sex. Once the RFI-growth period was finished, new groups were formed. Low RFI animals had observations less than 0.5 SD from the sample population's mean. The low RFI group consisted of 11 males and 11 females. The high RFI animals had observations greater than 0.5 SD from the sample population's mean. The high RFI group had 12 males and 12 females. The high and low groups' methane production was measured for six days via the SF_6 method (Johnson et al., 1994). When the methane production of the two groups was compared, no significant difference was found.

However, the authors also performed another RFI test on both the high- and low-RFI males, denoted RFI-met. The RFI-met trial lasted 32 days, including while the animals were being measured for methane production. Based on the new RFI measurements, the animals were re-grouped with 9 steers in the low-RFI category (negative RFI) and 14 steers in the high-RFI category (positive RFI). When the average methane production of each new group was compared (though the methane production of each animal was the same as the previous analysis), the low-RFI group had significantly less methane production than the high-RFI group ($P < 0.024$). The credibility of the latter analysis must be considered carefully because the RFI-met period was not long enough to provide an accurate measurement of RFI (BIF, 2018).

Like Mercadante et al. (2015), McDonnel et al. (2016) did not find any significant difference in methane production between high-RFI heifers and low-RFI heifers. Tellingly, there was no interaction effect between RFI and diet on methane production, but there was a significant effect for diet ($P < 0.001$). This further bolsters the idea that methane production is driven by the type of feed ingested (Johnson and Johnson, 1995).

Velazco et al. (2016) utilized records of 39 grazing yearlings to determine the relationship between daily methane production with mid-parent EBV for residual feed intake (RFI_{EBV}). The authors utilized a GEM (C-lock Inc., Rapid City, SD, USA) unit to measure methane production, and also predicted methane using the equation in Blaxter and Clapperton (1965). The authors also predicted DMI on pasture with the Minson and McDonald (1987) method. A moderate negative phenotypic correlation of -0.55 ($P < 0.01$) was noted between mid-parent RFI_{EBV} and observed methane emissions, thus the authors concluded that animals with more favorable RFI do not exhibit lower methane production. Further, the low-RFI cattle still had a higher predicted daily methane output after adjusting for live weight. Velazco et al.

(2016) did note the animals with lower mid-parent RFI_{EBV} were heavier, which increased the predicted DMI and, in turn, increased the predicted daily methane production of those animals.

Herd et al. (2016) also reported negative phenotypic correlations between methane production and RFI. The authors calculated three different RFI measurements: 1) observed RFI from a feedlot trial (RFI), 2) the average of the parent EBVs (RFI_{EBV}), and 3) the mid-parent EBV corrected for test weight ($RFI_{EBV\text{-}C}$). Each of these measurements was correlated to the methane production from the three phases of the trial: the feedlot, the grain-fed respiration chamber, and the roughage-fed respiration chamber. As shown in Table 1.4, only methane emissions from when the animals were fed roughages had any significant correlations with any RFI measurements (-0.37 with feedlot RFI, and -0.35 with RFI_{EBV}). Because animals with a low RFI_{EBV} were heavier on average in Herd et al. (2016), their weight may have confounded the results of the methane production analyses. When test weight was accounted for ($RFI_{EBV\text{-}C}$), no significant correlation was found. To explain the negative correlation between RFI and the roughage-fed chamber methane emissions, the authors put forth two explanations. First, lower RFI may not be associated with methane emissions in younger, growing animals. Alternatively, growing animals may have higher methane output per unit of feed intake.

The literature is divided as to whether methane production is positively or negatively correlated with RFI, or if the two are correlated at all. Therefore, more studies with sufficient statistical power and appropriate experimental design need to be conducted to determine the true nature of the association between methane production and residual feed intake.

Body Composition Traits

For the beef industry, body composition traits such as body fat and ribeye area determine yield and quality grades. These traits are important to consumer satisfaction and when marketing

on a quality grid. Two papers have investigated these relationships: Herd et al. (2014) and Donoghue et al. (2016). These studies reported very similar results, likely because the 777 animals analyzed by Herd et al. (2014) make up the majority of the 1046 animals analyzed by Donoghue et al. (2016).

Herd et al. (2014) used ultrasound to obtain measurements of rib fat, rump fat, and ribeye area (REA) on animals approximately 600 days in age. The Beef Improvement Federation (BIF) defines rib fat as the amount of subcutaneous fat between the 12th and 13th rib (2018). Rump fat is the measure of subcutaneous fat taken between an animal's hooks and pins (BIF, 2018). The ribeye area is a cross-sectional area of the longissimus dorsi between the 12th and 13th ribs (BIF, 2018). The phenotypic correlations between methane production and body composition traits were 0.13 (± 0.04) for rib fat, 0.17 (± 0.04) for rump fat, and 0.29 (± 0.04) for REA.

Donoghue et al. (2016) included the same measurements as Herd et al. (2014) but also incorporated intramuscular fat (IMF) collected via ultrasound. Phenotypic correlations between methane production and carcass traits were similar to those in Herd et al. (2014): 0.10 (± 0.4) for rib fat, 0.13 (± 0.04) for rump fat, 0.28 (± 0.03) for REA, and 0.15 (± 0.04) for IMF. The genetic correlation between methane production and rib fat was negligible at 0.11 (± 0.16). The correlation between methane production and rump fat was also not different from zero (0.10 ± 0.15). Alternatively, REA and IMF both showed a greater genetic correlation than the phenotypic correlation with methane emissions with 0.40 (± 0.16) and 0.36 (± 0.16), respectively.

Conclusion

Some genetic antagonisms exist between methane output and economically important traits, suggesting that selecting for reduced methane production directly would be detrimental to traits such as live weight and marbling. Alternatively, methane ratio traits have been created as a

way to select for animals that are most efficient in methane production. Using ratio traits, however, puts more selection emphasis on the trait with greater genetic variability and is an inefficient method of animal selection. Yet another option would be to select on animals with a negative residual methane phenotype. Much like negative RFI animals, negative residual methane animals produce less methane than expected. While residual methane has been shown to have few unfavorable correlations with economically important traits (Herd et al., 2016), this strategy has its own pitfalls. Chief among these is how to measure expected methane production as the most common method is through published regression equations predicting methane production from observed DMI. Furthermore, there is some concern in the scientific community whether selecting on a residual from regression would generate genetic gain. Ultimately, the best solution would be a well-constructed selection index and carefully planned breeding program to optimize selection on methane production while accounting for the economic balance between multiple economically relevant traits.

Methane Production and Genetic Loci

Single nucleotide polymorphisms (SNP) are variations at a single base pair in organism's genome. These variants can be associated with favorable traits, like reduced methane production. Selection programs utilizing genotypic information can greatly increase the rate of genetic change compared to phenotypic or even pedigree selection because incorporating SNP information improves the accuracy of genetic evaluations. Furthermore, genetic evaluations based on genotypes can be equally applied to any member of the population, from an embryo to a mature sire.

The earliest paper detailing SNP related to methane emissions was de Haas et al. (2011). Originally, 558 dairy heifers were sequenced for 54,001 SNP using the Illumnia 50k SNP panel.

After editing for SNP quality and prevalence, the authors were left with 548 animals and 43,011 SNP for each. Of those, only seven SNP were associated with predicted methane production (had a Bayes factor greater than 10.1, which was deemed to be the mathematical threshold for significance). The seven significant SNP all had small posterior probabilities, where a posterior probability is the likelihood a SNP is responsible for the trait of interest. The largest posterior probability (0.066) belonged to a SNP on chromosome 18. This SNP in particular explained a mere 0.2% of the total genetic variance for methane production. A SNP on chromosome 13 had the next highest posterior probability of 0.036. Despite the meager explanation of variation by each SNP individually, when direct genomic values were used in genetic predictions, the estimates were almost twice as accurate as pedigrees alone were used.

Pickering et al. (2015) preformed a similar analysis wherein the authors used predicted methane emissions on 731 dairy cattle and 48,957 quality-filtered SNP. The primary difference between the two studies was de Haas et al. (2011) predicted average methane production between weeks 1-27 of lactation, while Pickering et al. (2015) predicted weekly methane emissions over the course of a 44-week lactation. Because feed intake and, therefore, methane emissions change over time in lactating cows, weeks 10, 20, 30, 40, and 44 were chosen as the variables for an association analysis. They reported 35, 41, 33, 38, and 39 SNP markers that reached a significance threshold of $P < 0.001$ for weeks 10, 20, 30, 40, and 44, respectively. Eight SNP surpassed a higher significance threshold, $-\log_{10}(P)$ of 4, indicating the SNP had a large influence on predicted methane emissions during that week. Of those eight, one SNP located on chromosome 7 met the $-\log_{10}(P)$ significance threshold in every week. The average SNP effect across all weeks was -0.43 grams of methane per day. Although the two studies shared many similarities in their design and execution, none of the SNP identified by Pickering

et al. (2015) were reported as significant by de Haas et al. (2011). This implies methane production is a polygenic trait and has numerous SNP associated with it.

Manzanilla-Pech et al. (2016) used a different approach to identify SNP affecting methane production. In this study, the authors used three populations of cattle to achieve a multitude of goals: 1) identify SNP associated with methane traits in an Angus population, 2) validate those SNP across breed types utilizing a lactating Holstein population (POP1), and 3) ascertain if the SNP correlated with methane production in the Angus group correlated with SNP for DMI and live weight in a second Holstein population (POP2) from a previous study. The Angus population had methane measured in respiration chambers, while Holstein POP1 used the sulfur hexafluoride (SF_6) tracer technique. Two statistical thresholds were used to determine significance: the first was a strict $P < 0.001$ and the other was a more relaxed $P < 0.005$. Moreover, the authors utilized a false discovery ratio in order to approximate how many significant SNP may truly have an effect on the phenotype. In the Angus population, 3304 SNP met the $P < 0.005$ significance threshold and 803 surpassed the more conservative $P < 0.001$ limit. The false discovery ratios were 0.95 and 0.78, respectively. This implies only about 165-176 SNP have true associations with methane production. Single nucleotide polymorphisms of significance were scattered throughout the genome, but strong associations were seen on chromosome 2, 4, 12, 14, 20, and 30. When compared to de Haas et al. (2011) and Pickering et al. (2015), there is very little commonality. Disharmony in these papers may be due to the differences in measurement style, or it may be due to the differences in populations, e.g., breed and maturity. The one point of consensus is on chromosome 4, where Pickering et al. (2015) identified two significant SNP which match those identified by Manzanilla-Pech et al. (2016). For Holstein POP1, there were 2762 SNP were found to meet the liberal significance for

methane production and only 568 SNP exceeded the more stringent level. The false discovery ratios were not reported for this group. Few significant SNP for methane production were shared across breed. Only 23 SNP were shared between the Angus group and the Holstein POP1 at the more liberal significance threshold. The overlap dropped to 0 SNP between the Angus group and the more conservative threshold for Holstein POP1. Therefore, the authors concluded the SNP controlling methane production might be different across populations. As has already been established, both weight and DMI are highly genetically and phenotypically correlated with methane production. Because of this, Manzanilla-Pech et al. (2016) wanted to ascertain which SNP were shared between methane production, DMI and live weight in the Angus population. The authors discovered that 19% of significant SNP for methane production were also significant for live weight and dry matter intake. These SNP were located primarily on chromosomes 4, 12, and 14. Furthermore, some of the methane production loci identified by Manzanilla-Pech et al. (2016) were also associated with other traits in the literature.

Manzanilla-Pech et al. (2016) is not alone in identifying pleiotropic SNP associated with methane production. Pszczola et al. (2018) analyzed the breath of 287 Holstein cows for methane concentration through an infrared spectroscope, collected the animals' genotypes, and used Bayesian Variable Selection to perform a GWAS. Pszczola et al. (2018) identified 50 SNP associated with methane production that had a Bayes Factor greater than ten. Of those, three SNP had a Bayes Factor greater than 30, indicating very strong associations with methane production. In total, only 0.154% of the genetic variation in methane production was explained by these SNP. The lack of explanation may because of the limitations in the experimental design. Alternatively, it is also possible that methane's polygenic nature contributed to explaining a low percent of the genetic variation in the trait. Pszczola et al. (2018) identified 130 known genes as

candidates for influencing methane production but focused on the most promising five: CYP51A1 on BTA 4, PPP1R16B on BTA 13, and NTHL1, TSC2, and PKD1 on BTA 25. All of these genes are related to processes which influence the digestive tract. PKD1 in particular is linked to the development of the digestive tract. This suggests that PKD1 may directly or indirectly impact methane production by slightly altering the structural development of the rumen, thereby affecting methanogens by affecting the environment in which they live.

None of the genes Pszczola et al. (2018) singled out were corroborated by Calderon-Chagoya et al. (2019) when the latter performed a GWAS on 280 cattle. Calderon-Chagoya et al. (2019) set out to identify genomic locations associated with methane production in dairy and dual-purpose cattle in Mexico. Notably, this study measured methane production on *Bos taurus*, *Bos indicus*, and crossbreeds of the two utilizing a headbox. Calderon-Chagoya et al. (2019) reported that 46 of 21,958 SNP were significantly associated with methane emissions. Ten of these 46 SNP had been previously associated with milk traits, particularly fatty acid content. As these were dual-purpose animals, some SNP associated with methane production were also related to meat traits. Unsurprisingly, some SNP were found in quantitative trait loci (QTL) regions that have been associated with feed efficiency traits, such as DMI, RFI, and daily weight gain. More curiously, the authors also found markers located in QTLs associated with intramuscular fat and two different fatty acid concentrations.

Selection

Selection and mating are the two best tools in an animal breeder's toolkit. They are the means by which genetic changes in animal populations are made. Therefore, it is important to have the proper selection strategy to make the desired changes without losing much, if any, gains in other important traits.

Methane production has strong correlations with other economically important traits and with DMI in particular. As methane production decreases so does DMI, which also brings down live weight, milk production, and several other traits upon which the beef industry depends. Therefore, selecting animals based solely on methane production is generally not considered an effective strategy if producers want to remain profitable (Hegarty and McEwan, 2010; Herd et al., 2014). Instead, there a few tactics producers could use to reduce methane production without losing economic viability. One is to select on traits which may be related to methane production, but not to dry matter intake, such as residual feed intake. Another is to use ratio traits, like methane yield or methane intensity. However, the optimum strategy would be to use a selection index where methane production is just one of many traits.

Residual Feed Intake

Including residual feed intake as selection criterion in order to reduce methane production would provide several benefits over other mitigation strategies. For instance, some animal scientists believe low RFI bulls would ubiquitously reduce methane production throughout the industry, as opposed to a feed supplement mitigation approach which only reduce emissions in feed lots. More importantly, RFI has very few unfavorable associations with other traits, making it a safe target for indirect methane diminution. The amount of methane reduced would depend on the rate of adoption of RFI into an individual's breeding scheme and the selection pressure placed upon it. Both of these factors and their impact on methane abatement were quantified in Alford et al. (2006).

Alford et al. (2006) described a gene flow model which simulated the effects of improved RFI on methane production over the course of 25 years. It was assumed that breeding plans would not solely depend on reducing RFI, so a modest decrease of 0.08 kg dry matter per animal

per day was set as an annual rate of genetic change. In addition, it was also assumed all genetic change would come from sires with low RFI EBVs and replacement heifers would be selected for other traits. Another assumption the authors had to make was how quickly and to what extent RFI would be adopted into the Australian national herd's breeding plan. Based on estimates from previous literature, Alford et al. (2006) decided on a 30% maximum adoption percentage for the southern region and 15% maximum adoption in the northern area. Farms in the south were mainly composed of *Bos taurus* breeds, i.e., the breeds upon which RFI information was available for sires. The northern region had cattle heavily influenced by *Bos indicus* lines and it was assumed that region's maximum adoption percentage would be half that of the south. By the end of the simulation, the individual cow herd that selected for low RFI produced between 11.22-17.93% less CH_4 than the same herd in the starting year. The variation in production depended on the age of the cow as the sires of the younger cows had more genetic gain to pass on than the sires of the older cows. Furthermore, the youngest sires at the end of the simulation were producing 21.48% less methane than their unselected predecessors. The average individual 100-head herd in year 25 was producing 15.9% less methane than an unselected herd. Over the course of the simulation, the national herd saved 568,100 tons of methane, cumulatively. By year 25, the industry-wide savings was 60,900 tons annually, or a 3.1% reduction from the base year. Additionally, an increase in either annual genetic gain from additional selection pressure on the maternal side or adoption rate from a sustainability campaign would further reduce the amount of methane being produced. A 50% increase in genetic gain from the assumed decrease, 0.08 kg DM per head per day reduction to 0.12 kg DM per head per day reduction, would yield a year 25 reduction of 84,400; however, an increase in adoption rate, from 30% to 45% in the southern

herd and 15% to 22.5% in the northern herd, would reduce methane output by 91,300 tons annually in year 25 compared to the base year.

Ratio Traits

Methane yield (g CH_4/ kg DMI) and methane intensity (g CH_4/ kg product or g CH_4/ kg live weight) have both been proposed as possibilities measures of methane efficiency. The benefit of using a ratio trait is ratio traits spread out the selection pressure and thereby reduce any adverse effects that come with selecting for methane production directly. In other words, they are measures of efficiency rather than raw observations.

Donoghue et al. (2016) showed methane yield was either uncorrelated or very mildly correlated with economically important traits, either phenotypically or genetically. In particular, methane yield had no association with dry matter intake, circumventing the main problem of selecting upon methane production. Methane intensity has been less well studied, but according to results from Herd et al. (2013), this trait has negative associations with DMI and live weight. Both methane yield and methane intensity were shown to be heritable, estimates of 0.20 and 0.25, respectively (Manzanilla-Pech et al., 2016). Therefore, selection and genetic gain for either trait is possible.

One issue critics of ratio traits might point out is one way to reduce the ratio (which is favorable) is to increase the denominator. In other words, selecting on either methane yield or methane intensity traits would favor fast-growing, high-intake cattle, which may increase overall methane emissions per head. Another concern from a genetic standpoint is selection based on ratio traits can come with unintended consequences because it places higher than expected emphasis on the trait with higher genetic variance (Gunsett, 1984; van der Werf, 2004).

Residual Methane Traits

To prevent the uneven selection pressure ratio traits can cause, it may be more advantageous to use residual methane production instead. Residual methane production is the same idea as residual feed intake, observed measurement value minus the expected value calculated from an equation. In the case of residual methane production, smaller values are more favorable.

$$RMP_{ij} = O_i - E_j$$

where RMP_{ij} is the residual methane production of the i^{th} animal based on the j^{th} methane prediction equation, O is the observed methane production of the i^{th} animal, and E is the expected methane production based on the j^{th} methane prediction equation, such as IPCC Tier 2 (IPCC, 2019).

Residual methane traits and their associations were studied by Herd et al. (2014), Donoghue et al. (2016), and Manzanilla-Pech et al. (2016). The general conclusion was none of the residual methane traits showed any strong phenotypic association with DMI and the genetic correlations ranged from -0.25 to 0.10. The phenotypic correlations of residual methane traits and live weight were also modest, from -0.01 to 0.16. Each study varied in the ways the authors calculated expected methane, stretching from published equations to simple linear regressions to a trivariate analysis of DMI, live weight, and methane production. The assortment of tactics accounts for the range in correlation values. Nonetheless, the residual methane production based on the trivariate analysis performed by Manzanilla-Pech et al. (2016) proved to have the least impact DMI and live weight and should be the choice of animal breeders wanting to select on residual methane production.

The hidden difficulty of the residual methane production trait is in selecting the correct modeling equation and obtaining the required component data. As shown in the variability of the associations between residual methane production traits and dry matter intake, how one estimates expected methane could alter the selection decision being made. A decision regarding how to estimate methane would need to be finalized and implemented industry-wide for any enduring progress to be achieved.

Selection Index

A selection index is a form of multiple trait selection where each trait in the breeding objective receives an economic weight or measure of importance. Selection indices have been calculated in beef cattle with several objectives in mind. Two of the most common types of selection indices are maternal indices and terminal indices. A maternal index typically places emphasis on traits important for replacement heifers. On the other hand, a terminal index works on the assumption all offspring will be harvested and therefore puts all of the weighting on growth and carcass traits. Using a selection index is the most efficient and profitable way of selecting animals for breeding. Indices are also flexible and can be adjusted to suit new breeding goals, such as reducing methane emissions.

Wall et al. (2010) undertook a massive project to determine the effect of including methane production into the breeding goals of the United Kingdom (UK). The authors assessed six common breeding goals, three in sheep, two in beef cattle, and one in dairy cattle. For the purposes of this review, the focus will be on the objectives of the beef cattle segment. In the beef cattle segment, there were two indices, a terminal index and a maternal index, each with its own set of traits. The terminal index focuses on carcass traits like birth weight, 400-day weight, and ultrasonic fat depth. The maternal index includes carcass traits but puts a much larger emphasis

on maternal traits such as calving interval, gestation length, age first calving, and lifespan. Wall et al. (2010) first created a model to capture the range of methane production associated with differences in animal performance. This model was simply called the Genetic GHG model. The Genetic GHG model used the IPPC Tier 2 model (IPCC, 2006), where methane production was predicted from gross energy intake. The starting parameters for the GHG Genetic model were 100 breeding cows with a 600 kg liveweight that were primarily fed forages. Each herd had a 2% death rate and 3% open cow rate after the breeding season. Calves were assumed to be weaned at 210 days of age and slaughtered when they reached 600 kg. Of those calves, 98% of them were assumed to survive from weaning to slaughter. Because Wall et al. (2010) used the Tier 2 model (IPCC, 2006), it was assumed each animal consuming forage emitting 6.5% of its gross energy intake as methane, whereas each animal consuming concentrates over 90% emitted only 3% of its gross energy intake as methane. The authors fail to specify if the slaughter animals were grass-finished or grain-finished. In effect, Wall et al. (2010) used the Genetic GHG model as a basis on which to create an environmental index. The Genetic GHG model determined how much one unit of change in each selected trait would have on emissions. Then each trait received a weighting according to how great an effect changing each trait had and whether changing the trait increased or decreased methane emissions. As shown in Table 1.5, Wall et al. (2010) found improved fertility, e.g., a reduced age at first calving and calving interval, improved the environmental footprint of a maternally focused herd by reducing the number of unproductive days. In addition, a reduction in mature weight corresponded to less methane production because of the strong negative correlation between methane production and live weight (Herd et al., 2014). In the terminal herd (Table 1.6), Wall et al. (2010) reported improved carcass weight and feed efficiency, as measured by RFI, reduced GHG emissions. As weanling survival increased,

however, the percent of animals that survive from weaning to slaughter increased. Therefore, methane production also increased because more animals survived to produce methane. The contrast between increased fertility for replacement heifers in the maternal index but decreased weanling survival in the terminal index seems counter-intuitive; however, these new selection indices were developed to reduce methane, not to optimize profit as is the case for most indices. This is why looking beyond purely methane production is important. Strictly reducing methane might lead to unfavorable outcomes such as decreased beef production. In contrast, reducing emission intensity would encourage improvement in production traits while diluting the methane output. Therefore, it is often the case where producer profitability is better matched to breeding plans that lower emission intensity than breeding plans that aim to lower gross emissions.

Wall et al. (2010) did not stop at creating a stand-alone environmental index. The authors considered the standard selection index used in the UK. The standard index was developed to maximize profitability. Wall et al. (2010) then built a framework through which the standard index traits would receive different weightings in accordance with new environmentally focused breeding objectives. To combine the standard UK index with the environmental index developed by Wall et al. (2010), the first step was to establish the phenotypic and genetic parameters and correlations between the traits in the breeding goal. These were taken from a literature review conducted by another project (DEFRA, 2009). The next challenge was to translate environmental costs into economic terms. To accomplish this, Wall et al. (2010) used the shadow price of carbon. Here, the shadow price of carbon refers to the economic value of damages associated with methane emissions expressed as carbon dioxide equivalents (CO_2e; Price et al., 2007). To cover the range of uncertainty around the shadow price of carbon Wall et al. (2010) used four

different prices, resulting in four hybrid objectives. The shadow prices and how they were determined are listed here:

- CO_2£12: £12/t CO_2e, the approximate 2009 median price for the European allowance carbon units
- CO_2£26.50: £26.50/t CO_2e, the 2009 Shadow price of Carbon (SPC) from Price et al. (2007)
- CO_2£32.90: £32.90/t CO2e, the 2020 SPC from Price et al. (2007) chosen to represent a future price of carbon in 2-3 generations in sheep, beef and dairy. It is usual to forecast values when deriving index weights as the results of a selection decision today are expressed/realized in the future.
- CO_2£100: £100/t CO_2e, a worst-case scenario for price of carbon to ensure an adequate range for the results

Wall et al. (2010) examined the differences in trait weights for the standard objective, the environmental objective of reducing GHG per breeding cow (the gross emissions objective), the environmental objective of reducing GHG per kg of meat (the emission intensity objective), and the four hybrid objectives. As the breeding goal is altered from a purely economics-driven goal to goals which would also reduce methane emissions, different traits become more or less important. Mathematically, the more important a trait became in a given breeding objective, the further from zero its index weight became in that objective. As the breeding objective shifted focus from the standard objective to the gross emissions objective, selection became very focused increasing on 200-day weight, carcass weight, and calving interval (Table 1.7). Because larger animals consume more feed and thereby produce more methane (Herd et al., 2014), selecting for heavier terminal offspring (200-day weight and carcass weight) increased methane

production in the short-term, but that is balanced by decreasing mature cow size which lessened methane in the long-term. This can physically be achieved by selecting for large, terminal sires, but more moderate-sized replacement females. Moreover, an increased calving interval decreased the number of cattle produced overall which decreased the amount of methane produced, though this has the downside of also creating less profit for producers. The gross emissions objective was also weighted against high-RFI, which contributed to greater methane production per animal as demonstrated by Nkrumah et al. (2006) and Hegarty et al. (2007). The intensity objective was more restrained in its weightings of maternal cow traits. It only put a mild positive weighting on 200-day weight and carcass weight. This objective weighted against high mature weights and high RFI values, but to a much more subtle degree. In contrast to the gross emissions objective, the intensity objective was weighted to decrease the calving interval and age at first calving. Notably, the authors set the weightings of many of the other traits included in the standard index to zero in the environmentally focused objectives. For example, carcass condition scores, gestation length, calving difficulties, and lifespan all received zero weightings. The hybrid objective with the lowest carbon price, Eco+ CO_2£12, had weightings very similar to those of the standard objective, save the hybrid objective put some weighting on RFI. As the carbon price increased, less weight was put on keeping the calving interval low while more weight was put on increasing 200-day weight and carcass weight. Interestingly, the traits that received zero weighting in the environmental objectives, carcass condition scores, gestation length, calving difficulties, and lifespan, had the same weightings in all the hybrid objectives as they had in the standard objective. It is important to keep in mind the hybrid objectives had a partial focus on producer earnings which translates to pounds of sellable beef. As the weightings in each objective changed in accordance with the breeding goal, the response in traits changed

with them. However, the traits in the selection indices were not the only ones to change. The selection indices used in Wall et al. (2010) relied on the correlations between traits to indirectly select against methane production and the repercussions are shown in Table 1.8. Curiously, the standard objective was better at reducing mature weight than the environmentally focused objective. However, the environmental objectives led to a greater increase in carcass weight. Moreover, as methane production began to play a larger role in the breeding objective, gestation length increased while RFI decreased. Wall et al. (2010) had similar results for the terminal index to those found in the maternal index. The index weightings for the terminal index are shown in Table 1.9. As in the maternal index, carcass weight received a large weighting under the gross emissions objective. However, in that same objective, weanling survival was actually selected against. On the contrary, the intensity objective placed very little emphasis on any traits in the terminal index. As in the maternal index, the hybrid breeding objectives began weighted similarly to the standard objective when the shadow price of carbon is low, but then grew closer to the gross emission objective weightings as the price increased. In the terminal index the weightings for even the highest shadow price of carbon were much closer to the weightings under the standard objective than the weightings under the gross emissions objective. This indicates that current paradigms would have to radically shift before the beef industry switched to primarily focusing on methane reduction. When Wall et al. (2010) examined the trait responses in the terminal index under different breeding objectives, the author found the environmental focused objectives actually increased carcass weight more than the standard objective (Table 1.10). In addition, the environmental objectives decreased RFI, a favorable result. However, not all responses were favorable. Wall et al. (2010) also calculated increased carcass fat score, gestation length, and calving difficulty while decreased carcass condition score,

all of which producers would prefer to avoid. In summary, Wall et al. (2010) showed methane production could be incorporated into selection indices already in use and would have some measurable effect. This idea was further expanded upon in Lopez-Paredes et al. (2018), wherein the authors used a population of Spanish Blonde d'Aquitaine as a case study.

Lopez-Paredes et al. (2018) used records from the Spanish Breeders Association of Blonde d′Aquitaine in order to calculate means, variances, and genetic parameters for maternal traits like calving interval and age at first calving, as well as terminal traits like carcass weight and growth. The authors of Lopez-Paredes et al. (2018) used the IPCC Tier 2 (2006) mode, in combination with gross energy intake estimates from previous literature to approximate methane production. The authors approximated methane production for both the average breeding cow and the average feedlot animal and expressed those values as kg of CH_4 per slaughtered calf per year. Lopez-Paredes et al. (2018) modeled three breeding objectives. The first was a benchmark scenario where profits were optimized, and methane production was not included in the breeding goal. The second scenario implemented a carbon tax of 1.22€/kg CH_4. This was very similar to the hybrid objectives of Wall et al. (2010). However, the shadow price of carbon in Lopez-Paredes et al. (2018) was assumed to be equivalent to roughly 48.89£/t CO_2e, between the highest and second-highest carbon prices modeled by Wall et al. (2010). Finally, the last scenario considered by Lopez-Paredes et al. (2018), was a carbon quota. In this objective, meat production traits were optimized while methane production was held constant. The intensity index in Wall et al. (2010) mirrors the quota scenario, in that the goal of both was to find the balance between meat production and methane production. It is also worth noting Lopez-Paredes et al. (2018) assumed the amount of methane would be kept constant by varying the number of animals while the amount of product would continue to increase via means of selecting for more

efficient animals. The economic weights of the traits in the selection indices in each scenario were based on a bioeconomic profit function developed by Lopez-Paredes et al. (2017). The basic function would determine profit per year. The index weights were defined as the partial derivative of the profit function with respect to the trait considered and expressed as euros per slaughtered calf per year. Modifications were made to each function, depending on which objective was being met. The simplest index weight equation was used for the benchmark objective:

$$EV_i = \partial((I - FAT - PROD) \bullet c_s)/\partial x_i$$

where EV_i is the index weight of trait *i*, I is the income per slaughtered calf, FAT is the cost of the finishing calves to meet their energy requirements in the feedlot until a fixed age of slaughter, PROD is the cost of production per slaughtered calf, including feeding cost of heifers, cows, and culled cows to meet their energy requirements minus income per culled cow carcass at sale, c_s is 365 divided by the age of calf at slaughter, and x_i is the value of trait *i*.

For the carbon tax objective, Lopez-Paredes et al. (2018) used the following equation:

$$EV_i = \partial((I - FAT - PROD) \bullet c_s - (t \bullet (M_{cow} + M_{calf})))/\partial x_i$$

where EV_i is the index weight of trait *i*, I is the income per slaughtered calf, FAT is the cost of the finishing calves to meet their energy requirements in the feedlot until a fixed age of slaughter, PROD is the cost of production per slaughtered calf, including feeding cost of heifers, cows, and culled cows to meet their energy requirements minus income per culled cow carcass at sale, c_s is 365 over the age of calf at slaughter, *t* is the rate of carbon tax (1.22€/kg CH_4), M_{cow} is the kg of methane per slaughtered calf per year for cows, replacement heifers, and cull cows, M_{calf} is the kg of methane per slaughtered animal per year for feedlot animals, and x_i is the value of trait *i*.

Finally, the equation for the carbon quota objective restricted the amount of progress that could have been made in every given trait by how much the change in the trait would change the amount of methane produced.

$$EV_i = \frac{\partial((I - FAT - PROD) \bullet c_s}{\partial x_i} - \left((I - FAT - PROD) \bullet c_s\right) \bullet \frac{\frac{\partial(M_{cow} + M_{calf})}{\partial x_i}}{M_{cow} + M_{calf}}$$

where EV_i is the index weight of trait *i*, I is the income per slaughtered calf, FAT is the cost of the finishing calves to meet their energy requirements in the feedlot until a fixed age of slaughter, PROD is the cost of production per slaughtered calf, including feeding cost of heifers, cows, and culled cows to meet their energy requirements minus income per culled cow carcass at sale, c_s is 365 over the age of calf at slaughter, M_{cow} is the kg of methane per slaughtered calf per year for cows, replacement heifers, and cull cows, M_{calf} is the kg of methane per slaughtered calf per year for feedlot animals, and x_i is the value of trait *i*.

With the profit equations developed for each breeding objective, Lopez-Paredes et al. (2018) was able to compute the selection index weights for each objective. In the benchmark objective, 48% of the selection weight was placed on cow traits, while 52% was placed on calf traits. As can be seen in Table 1.11, increasing carcass weight gain and decreasing mature weight were the highest priorities for the benchmark objective. Under the carbon tax objective, selection pressure was shifted away from calf growth to improving cow traits. The importance of cow traits increased because shorter non-productive lengths, like calving intervals, also imply less methane production per slaughtered calf per year. In addition, this objective also places 4.9% of the index weight on methane traits, the greatest emphasis of all objectives. In contrast to the carbon tax objective, the carbon quota objective placed more emphasis on calf traits than cow traits. This was because carcass weight gain in particular was highly heritable and greatly

increased the income portion of the profit equation upon which all index weights were based. The carbon quota objective also considered methane traits, but to a smaller degree (1.8%) than the carbon tax objective. In general, all objectives were similar in a few key respects with the differences being mostly in magnitude. For example, in all objectives, mature weight, age at first calving, calving interval, and calving ease all received negative index weights because decreases in those traits not only reduced costs of production but also reduced methane production per slaughtered calf per year. Conversely, weaning weight, carcass gain, carcass confirmation score, and cull cow carcass weight all received positive index weights because they all increased the amount of income seen by operations. The response seen in traits under the three breeding objectives was expressed both in the units of the trait and as euros per slaughtered calf per year (Table 1.12). The benchmark objective showed 97% of the genetic response profit was derived from improved calf traits which increased profit. Reducing calving interval and age at first calving also increased profit, but to a lesser degree. However, because larger cows require more feed to meet their needs and this objective allowed for the largest cows, the benchmark scenario cited an increased mature weight as its largest genetic cost. Despite the larger mature weight, the benchmark scenario actually showed a decrease in methane production for the cow herd. This reduction is likely due to the decrease in non-productive days which increased the number of slaughtered calves per year, consequently decreasing the ratio of kg CH_4 per slaughtered calf per year. The total profit of this objective was 68.84€ per slaughtered calf per year. The profitability of the carbon tax objective fell to 60.98€ per slaughtered calf per year, not only because methane production itself was a cost, but also because calf traits were not selected for as intensely as in the benchmark objective and a beef operation's revenue would not be as great. In an attempt to limit the amount of methane being produced by reducing the size of both cows and calves, this

objective also limited the amount of product produced. The final objective, the carbon quota objective, actually improved profitability over the benchmark objective. The carbon quota objective selected for slightly smaller mature cows with slightly improved fertility (age at first calving and calving interval) as compared to the benchmark scenario. Those minute changes lead to not only improved profitability by decreased costs, but also to lower methane emissions per animal than in the benchmark scenario. However, the increased profit per animal is balanced with the assumption of fewer animals in order to cap the amount of methane produced. Lopez-Paredes et al. (2018) concluded adding methane traits to the breeding goal will affect the future type of beef animal. Moreover, the inclusion of methane in the breeding objective would affect producer profitability by either reducing the amount of meat produced or reducing the number of animals available in order to hold methane at a constant level. None of the scenarios modeled by Lopez-Paredes et al. (2018) considered the social implications of reducing methane. Lopez-Paredes et al. (2018) recommended all genetic, economic, and social facets should be carefully weighed before any decisions are set by policy makers.

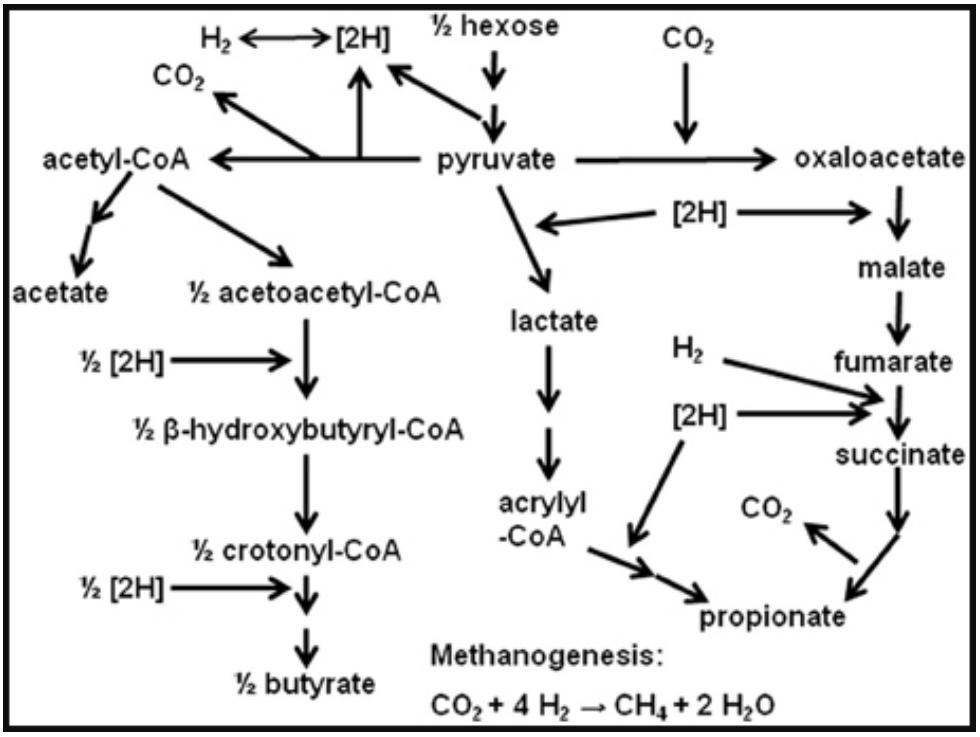
Selection indices are the most efficient selection tools producers have available. They allow for an optimization of multiple trait selection and can be customized for almost any breeding goal. While methane production is not included in any national breeding objectives at the moment, under certain market conditions, such as carbon taxes or carbon quotas, selection indices can be adapted to accommodate these forces (Wall et al., 2010; Lopez-Paredes et al., 2018). In fact, given the right market forces, selection indices can be leveraged to increase profitability while simultaneously decreasing methane production of beef operations (Lopez-Paredes et al., 2018).

Conclusion

In terms of choosing the correct trait for a breeding scheme, the decision depends on the breeding objective. An overall reduction in methane emissions may be achieved by directly selecting against methane production or by selecting for lower RFI. Alternatively, cattle selected on methane yield or intensity would increase methane production per head but could lower overall emissions by producing fast-growing animals and meeting demands with fewer cattle. Residual methane production traits would focus on the animals producing less methane than expected, which may or may not reduce overall methane emissions but would increase the efficiency of each animal. Finally, the optimal solution may be selection indices. Selection indices would incorporate methane production traits into a model with the correlation of other traits already considered. Additionally, selection indices could be made for a variety of scenarios and producers would be able to select of index appropriate from their needs. However, selection indices require the direct measurement of methane production on a large number of animals which is a logistical hurdle at the present time. Regardless of the selection methodology, it is possible to reduce methane production through breeding which would result in sustained and cumulative benefits to the beef industry as a whole.

Figure 1.1

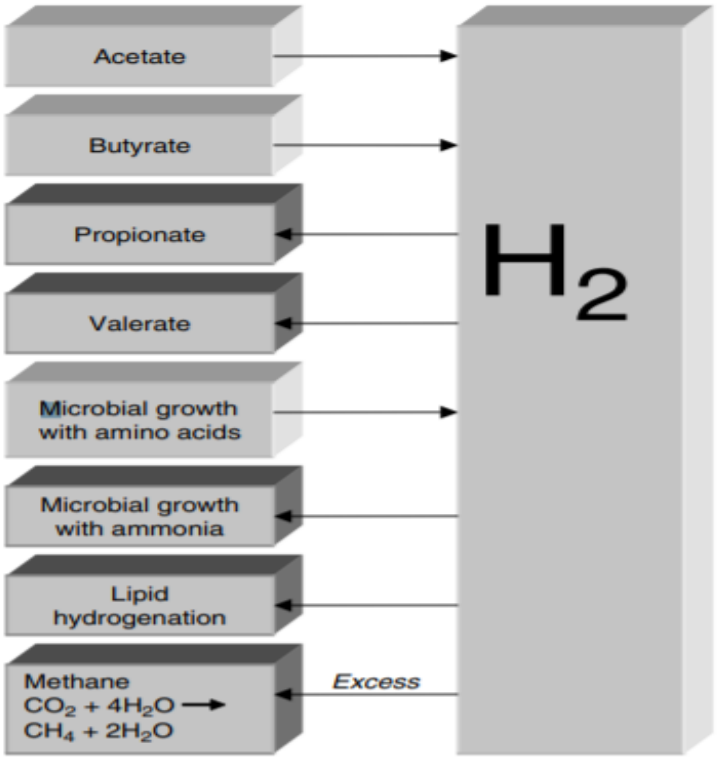
Main ruminal pathways where free hydrogen is used or released



Adapted from Ungerfeld, 2013

Figure 1.2

Sources and sinks of hydrogen during ruminal fermentation



Adapted from Kebreab et al., 2004

Table 1.1

Empirical models for estimating enteric methane from ruminant animals

Equation	**Reference**
7.42 + 94.28 * DMI[a] (kg/d) * 0.05524 (MJ/g CH_4)	Kriss, 1930
-2.07 + 2.636 * DMI[a] (kg/d) -0.105 * DMI[a] $(kg/d)^2$	Axelsson, 1949
5.447 + 0.469 * (energy digestibility at maintenance intake, % of GE[b]) + multiple of maintenance * (9.930 - 0.21 * (energy digestibility at maintenance intake, % of GE[b]))/100 * GEI[c] (MJ/d)	Blaxter and Clapperton, 1965
4.38 (±1.46) + 0.0586 (±0.0175) * MEI[d] (MJ/d)	Ellis et al., 2007
North American dairy cattle milking 8400 kg milk/head/yr.: 138 kg CH_4/head/yr. All other North American cattle: 64 kg CH_4/head/yr.	IPCC, 2019
[0.07 *GEI[c]]/0.05565 *Alternatively* Cattle fed ≥85% concentrate: 4.0% ± 1.0% of GEI[c] Cattle fed < 85% concentrate: 7.0% ± 1.0% of GEI[c]	IPCC, 2019
0.341 + 0.511 * NSC[e] (kg/d) + 1.74 * HC[f] (kg/d) + 2.652 * CEL[g] (kg/d)	Moe and Tyrrell, 1979
56.27 – (56.27 + 0) * e^(-0.028 * DMI[a] (kg/d))	Mills et al., 2003

a = dry matter intake
b= gross energy
c= gross energy intake
d= metabolizable energy intake
e= non-structural carbohydrate
f= hemicellulose
g= cellulose

Table 1.2

Summary of heritabilities estimates for methane production in beef and dairy cattle

Heritability ± SE	Population	Methane Measurement Type	Study
0.17 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.15 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.26 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.22 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.07 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.36 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.35 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.52 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.52 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.37 ± 0.11	Dual Purpose	Prediction	Kandel et al. (2012)
0.35 ± 0.12	Dairy	Prediction	de Haas et al. (2011)
0.13 ± 0.04	Dairy	Prediction	Pickering et al. (2015)
0.24 ± 0.01	Dairy	Prediction	Kandel et al. (2017)
0.25 ± 0.01	Dairy	Prediction	Vanrobays et al. (2016)
0.47 ± 0.07	Beef	Prediction	Sobrinho et al. (2015)
0.32 ± 0.07	Beef	Prediction	Sobrinho et al. (2015)
0.19 ± 0.05	Beef	Prediction	Manzanilla-Pech et al. (2016)
0.15 ± 0.05	Beef	Prediction	Manzanilla-Pech et al. (2016)

0.21 ± 0.06	Dairy	Direct	Laasen and Løvendahl (2016)
0.25 ± 0.16	Dairy	Direct	Lassen et al. (2016)
0.24 ± 0.15	Dairy	Direct	Lassen et al. (2016)
0.23 ± 0.23	Dairy	Direct	Manzanilla-Pech et al. (2016)
0.24 ± 0.06	Beef	Direct	Arthur et al. (2016)
0.18 ± 0.06	Beef	Direct	Arthur et al. (2016)
0.27 ± 0.07	Beef	Direct	Arthur et al. (2016)
0.19 ± 0.06	Beef	Direct	Arthur et al. (2016)
0.20 ± 0.05	Beef	Direct	Hayes et al. (2016)
0.18 ± 0.05	Beef	Direct	Hayes et al. (2016)
0.30 ± 0.06	Beef	Direct	Manzanilla-Pech et al. (2016)

Adapted from Brito et al. (2018)

Table 1.3

Phenotypic and genetic correlations (standard error) between methane production and body weight in beef cattle

Trait	Herd et al. (2014)		Donoghue et al. (2016)	
	Phenotypic	*Genetic*	*Phenotypic*	*Genetic*
Birth Weight	0.19 (0.05)	NA	0.26 (0.04)	0.36 (0.18)
Weaning Weight	0.50 (0.04)	NA	0.53 (0.03)	0.84^{d} (0.09) /0.32^{m} (0.19)
Yearling Weight	0.57 (0.03)	NA	0.61 (0.09)	0.86 (0.06)
Finished Weight	0.49 (0.05)	NA	0.56 (0.03)	0.79 (0.08)

d=direct weaning weight
m=maternal weaning weight

Table 1.4

Correlations between different quantifications of residual feed intake (RFI) and measurements of methane production (CH4) under various circumstances

	Feedlot RFI[a]	RFI_{EBV}[b]	RFI_{EBV-C}[c]
Feedlot CH_4	-0.05	-0.09	0.08
Grain chamber CH_4	-0.05	-0.04	0.01
Roughage chamber CH_4	-0.37*	-0.35*	-0.15

[a]RFI measured under feedlot conditions with a high grain diet
[b]RFI for an individual expressed as the average of the parent's expected breeding value for RFI
[c] RFI for an individual expressed as the average of the parent's expected breeding value for RFI corrected for body weight
*P < 0.05
Adapted from Herd et al., 2016

Table 1.5

Greenhouse gas (GHG) values for maternal cattle with discounted genetic expressions and the GHG weights for each goal trait. Positive trait values indicate a decrease in GHG emissions

Trait	GHG value (-1*kg CO_2e/breeding cow/ unit change in trait)	Discounted genetic expression (per breeding cow)	GHG index weight (-1*kg CO_2e /breeding cow)
Calving interval (days)	7.46	0.774	5.77
Age at first calving (days)	3.85	0.141	0.54
Maternal 200-day weight (kg)	8.80	0.654	5.76
Mature weight (maintenance) (kg)	-0.878	0.774	-0.68
Mature weight (replacement) (kg)	-1.89	0.141	-0.27
Mature weight (combined) (kg)			-0.95
Carcass weight (kg)	12.26	0.680	8.34
RFI of breeding animals (kg of DMI/day)	0.43	0.774	0.33
RFI of growing animal (kg of DMI/day)	0.38	0.680	0.26

*RFI is residual feed intake; DMI is dry matter intake; CO_2e is carbon dioxide equivalent
Adapted from Wall et al., 2010

Table 1.6

Greenhouse gas (GHG) values for terminal cattle with discounted genetic expressions and the GHG weights for each goal trait. Positive trait values indicate a decrease in GHG emissions

Trait	GHG value (-1*kg CO2e/breeding cow/ unit change in trait)	Discounted genetic expression (per breeding cow)	GHG index weight (-1*kg CO2e /breeding cow)
Carcass weight (kg)	12.26	0.430	5.27
Residual feed intake of growing animal	0.38	0.430	0.16
Weanling survival	-16.54	0.654	-10.82

*CO_2e is carbon dioxide equivalent
Adapted from Wall et al., 2010

Table 1.7

Selection index weights used in maternal beef when seven different breeding objectives were selected:
Standard set of economic weights (Standard); Environmental weights expressed per breeding cow (Gross Emissions); Per kilogram of meat (Emission Intensity); Combined economic and environmental weights at four carbon prices (Eco+CO_2£)

	Breeding objectives and selection index weights						
	Standard (£)	**Gross Emissions (kg CO_2e)**	**Emission Intensity (kg CO_2e / kg meat)**	**Eco+ CO_2£12 (£)**	**Eco+ CO_2£26 (£)**	**Eco+ CO_2£32.90 (£)**	**Eco+ CO_2£100 (£)**
Trait names							
200-day weight	0.73	5.75	0.05	0.80	0.88	0.92	1.31
Carcass weight	0.70	8.34	0.07	0.80	0.92	0.97	1.53
Carcass condition score	6.70	0	0	6.70	6.70	6.70	6.70
Gestation length direct	-1.17	0	0	-1.17	-1.17	-1.17	-1.17
Calving ease direct	-2.88	0	0	-2.88	-2.88	-2.88	-2.88
Calving ease maternal	-2.19	0	0	-2.19	-2.19	-2.19	-2.19
Calving interval	-0.83	5.77	-0.01	-0.76	-0.68	-0.64	-0.25
Age at first calving	-48.11	0.54	-0.002	-48.10	-48.10	-48.09	-48.10
Lifespan	6.63	0	0	6.63	6.63	6.63	6.63
Mature weight	-0.23	-0.95	-0.01	-0.24	-0.26	-0.26	-0.33
RFI growing	0	-0.26	-0.002	-0.003	-0.01	-0.01	-0.03

animals							
RFI breeding animals	0	-0.33	-0.003	-0.004	-0.01	-0.01	-0.03

*RFI is residual feed intake; CO_2e is carbon dioxide equivalent
Adapted from Wall et al., 2010

Table 1.8

Index and correlated trait responses for maternal beef index when seven different breeding objectives were selected:
Standard set of economic weights (Standard); Environmental weights expressed per breeding cow (Gross Emissions); Per kilogram of meat (Emission Intensity); Combined economic and environmental weights at four carbon prices (Eco+CO_2£)

	Breeding objectives and trait responses (in trait units per annum)						
	Standard	**Gross Emissions (kg CO_2e)**	**Emission Intensity (kg CO_2e / kg meat)**	**Eco+ CO_2£12**	**Eco+ CO_2£26**	**Eco+ CO_2£32.90**	**Eco+ CO_2£100**
Trait names							
200-day weight maternal (kg)	0.168	0.009	0.000	0.157	0.146	0.141	0.103
Carcass weight (kg)	2.699	3.548	3.684	2.855	3.001	3.054	3.361
Carcass condition score (1-4)	0.031	0.018	0.018	0.030	0.030	0.030	0.027
Gestation length-direct (days)	-0.050	0.022	0.017	-0.044	-0.038	-0.036	-0.018
Calving interval (days)	-0.711	0.317	-0.448	-0.632	-0.546	-0.512	-0.256
Age at first calving (days)	-0.005	-0.010	-0.005	-0.005	-0.006	-0.006	-0.008
Lifespan (number of lactations)	0.037	0.012	0.015	0.035	0.034	0.033	0.027
Mature weight (kg)	-3.505	0.449	-0.079	-3.221	-2.912	-2.787	-1.827

RFI growing animals (kg of DMI/ day)	-4.020	-9.931	-10.432	-4.700	-5.377	-5.634	-7.339
RFI breeding animals (kg of DMI/ day)	-4.092	-7.489	-7.386	-4.531	-4.960	-5.121	-6.152

*RFI is residual feed intake; DMI is dry matter intake; CO_2e is carbon dioxide equivalent
Adapted from Wall et al., 2010

Table 1.9

Selection index weights used in terminal beef index when seven different breeding objectives were selected:
Standard set of economic weights (Standard); Environmental weights expressed per breeding cow (Gross Emissions); Per kilogram of meat (Emission Intensity); Combined economic and environmental weights at four carbon prices (Eco+CO_2£)

	Breeding Objectives and selection index weights						
	Standard (£)	**Gross Emissions (kg CO_2e)**	**Emission Intensity (kg CO_2e / kg meat)**	**Eco+ CO_2£12 (£)**	**Eco+ CO_2£26 (£)**	**Eco+ CO_2£32.90 (£)**	**Eco+ CO_2£100 (£)**
Trait names							
Carcass weight	1.20	5.27	0.04	1.26	1.34	1.37	1.73
Carcass fat score	-6.00	0	0	-6.00	-6.00	-6.00	-6.00
Carcass condition score	7.00	0	0	7.00	7.00	7.00	7.00
Gestation length direct	-1.00	0	0	-1.00	-1.00	-1.00	-1.00
Calving difficulty direct	-2.88	0	0	-1.00	-2.88	-2.88	-2.88
RFI of growing animals	0	-0.16	-0.002	-0.002	-0.004	-0.01	-0.02
Survival from birth to wean	0	-10.82	0.05	-0.13	-0.29	-0.36	-1.08

*RFI is residual feed intake; CO_2e is carbon dioxide equivalent
Adapted from Wall et al., 2010

Table 1.10

Index and correlated trait responses for terminal beef index when seven different breeding objectives were selected:
Standard set of economic weights (Standard); Environmental weights expressed per breeding cow (Gross Emissions); Per kilogram of meat (Emission Intensity); Combined economic and environmental weights at four carbon prices (Eco+CO_2£)

Breeding objectives and trait responses (in trait units per annum)

	Standard	**Gross Emissions (kg CO_2e)**	**Emission Intensity (kg CO_2e / kg meat)**	**Eco+ CO_2£12**	**Eco+ CO_2£26**	**Eco+ CO_2£32.90**	**Eco+ CO_2£100**
Trait names							
Carcass weight	2.317	2.514	2.504	2.343	2.370	2.380	2.454
Carcass fat score	-0.035	0.047	0.048	-0.031	-0.027	-0.025	-0.011
Carcass condition score	0.063	0.033	0.032	0.062	0.060	0.060	0.055
Gestation length - direct	0.016	0.068	0.066	0.019	0.022	0.023	0.033
Calving difficulty - direct	0.005	0.012	0.012	0.005	0.006	0.006	0.007
RFI of growing animals	-2.721	-8.743	-9.006	-3.039	-3.386	-3.528	-4.685
Shear force	-0.001	-0.001	-0.001	-0.001	-0.001	-0.001	-0.001
Birth Survival	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Survival from birth	0.000	0.000	0.000	0.000	0.000	0.000	0.000

to wean							
Docility score	0.009	0.006	0.006	0.009	0.009	0.009	0.009

Adapted from Wall et al., 2010

Table 1.11

Economic weights of three breeding objectives per unit of increase of each trait in euros per slaughtered calf per year (€/sc/year) and per additive standard deviation (€/sc/year/σ_a), relative importance (RI)

		Benchmark			**Carbon Tax**			**Carbon Quota**		
		€/SC /year	€/SC /year/σ_a	RI (%)	€/SC /year	€/SC /year/σ_a	RI (%)	€/SC /year	€/SC /year/σ_a	RI (%)
Cow Traits										
	Mature weight	−0.5	−25.15	18.7	−0.6	−30.27	18.2	−0.47	−23.73	18.1
	Age at first calving	−0.13	−12.13	9.0	−0.16	−14.60	8.8	−0.13	−11.4	8.7
	Calving interval	−1.39	−10.85	8.1	−1.65	−27.36	16.4	−1.31	−10.25	7.9
	Calving ease maternal	−14.16	−6.49	4.8	−16.76	−7.68	4.6	−13.42	−6.15	4.7
	Weaning weight maternal	0.2	2.37	1.4	0.25	2.91	1.7	0.12	1.38	1.1
	Cull cow carcass conformation score	3.16	2.88	2.1	3.16	2.88	1.7	3.16	2.88	2.2
	Cull cow conformation score	0.14	4.77	3.6	0.11	3.91	2.3	0.11	3.99	3.1
Calf Traits										
	Calving ease	−14.16	−12.58	9.4	−16.76	−14.89	8.9	−13.42	−11.93	9.1
	Weaning weight	0.2	3.02	2.3	0.25	3.75	2.2	0.12	1.77	1.3
	Carcass conformation	19.40	12.27	9.1	19.4	12.27	7.4	19.40	12.27	9.4

	score									
	Carcass weight gain	0.782	41.65	31.0	0.713	38.0	22.8	0.802	42.69	32.6
Methane Traits										
	Calf sector methane	-	-	-	−1.22	−3.68	2.2	−0.34	−1.03	0.8
	Breeding cow sector methane	-	-	-	−0.54	−4.56	2.7	−0.16	−1.35	1.0

Adapted Lopez-Paredes et al., 2018

Table 1.12

Annual genetic change traits in three breeding objectives expressed in unit of trait (parenthesis) and in euros per slaughtered calf per year (€/sc/year)

		Benchmark		**Carbon Tax**		**Carbon Quota**	
		Change in trait	€/sc/year	Change in trait	€/sc/year	Change in trait	€/sc/year
Cow Traits							
	Mature weight (kg)	6.75	−3.37	−0.84	0.50	6.27	−2.95
	Age at first calving (days)	−12.03	1.56	−10.32	1.65	−12.80	1.66
	Calving interval (days)	−2.73	3.79	−2.61	4.30	−2.76	3.61
	Calving ease maternal (1-4)	0.00	−0.06	0.00	−0.08	0.00	−0.06
	Weaning weight maternal (kg)	−3.88	−0.78	−3.26	−0.81	−4.10	−0.49
	Cull cow carcass conformation score (1-15)	0.12	0.38	0.15	0.47	0.14	0.39
	Cull cow conformation score (kg)	4.68	0.66	−0.58	−0.06	4.36	0.48
Calf Traits							
	Calving ease (1-4)	0.04	−0.59	0.04	−0.70	0.04	−0.56
	Weaning weight (kg)	4.16	0.83	2.42	0,61	3.84	0.46
	Carcass conformation	0.38	7.47	0.40	7.74	0.38	7.43

	score (1 -15)						
	Carcass weight gain (g/day)	75.58	58.95	70.90	50,55	75.30	60.39
Methane Traits							
	Methane from calf during fattening (kg)	2.91	−	2.38	−2.90	2.81	−0.95
	Methane from breeding cows (kg)	−0.30	–	−0.53	0.29	−0.84	0.07
Profit		68.84		60.98		69.48	

Adapted Lopez-Paredes et al., 2018

Chapter 2 - Genetic Evaluation of Methane Traits Estimated by Different Methane Prediction Equations

Abstract

Enteric methane is a potent greenhouse gas and represents an inefficiency in the ruminant digestive system. Genetic selection offers a permanent and cumulative opportunity to diminish enteric methane emissions as long as selection pressure is maintained. Logistic and monetary difficulties in directly measuring methane emissions can make the genetics evaluation on a proxy trait like predicted methane production a more feasible option, while understanding that inclusion of genotyping data can allow for quicker genetic progress. Thus, three predicted methane production traits were calculated for 830 crossbred steers fed in seven groups. The methane prediction equations used included models from Ellis et al. (2007), Mills et al. (2003), and IPCC (2019). Pearson correlations between the traits were all greater than 0.99, indicating that each prediction equation behaved similarly. Further, the Spearman correlations between the estimated breeding values for each trait were also 0.99, which suggests any of the predicted methane traits could be used without substantially changing the selection candidates. The heritabilities of Ellis predicted methane production, Mills predicted methane production, and IPCC predicted methane production were 0.71, 0.74, 0.70, respectively. No single nucleotide polymorphism reached the threshold for significance for any of the traits. Nonetheless, the SNP closest to the significance threshold indicate genes related to collagen, intracellular microtubules, and DNA transcription may play a role in predicted methane production or its component traits.

Introduction

Ruminant animals eructate enteric methane as by-product of their digestive process. Methane is a greenhouse gas that has 84 times more global warming potential than carbon-dioxide over a 20-year timeframe (Myhre et al., 2013). Further, enteric methane represents an inefficiency of the ruminant system. Anywhere from 2-12% of energy consumed by cattle is emitted as methane (Johnston and Johnston, 1995).

Phenotypic and genetic variation in methane production between animals has been reported (Blaxter and Clapperton, 1965: Herd et al., 2016; Renand et al., 2019), which implies reduction of methane emissions through breeding is possible. Breeding for methane reduction offers several benefits that other methods like feed additives and methane inoculants (covered extensively in Beauchemin et al., 2020) do not; namely, that genetic improvements are permanent and cumulative as long as selection pressure on the trait of interest is maintained. The drawback for selecting for animals solely based on methane production is the fact methane production is genetically and phenotypically correlated to dry matter intake (DMI) and body weight (Herd et al., 2014). This means selecting for reduced methane production directly could also reduce DMI and body weight.

Several studies have been conducted to determine quantitative trait loci (QTL) associated with predicted methane production. One of the first studies to examine the single nucleotide polymorphisms (SNP) was de Haas et al. (2011), where the authors predicted methane emission of 665 Holstein cattle. Seven significant SNP were on 5 chromosomes (chromosomes 13, 18, 24, 26, and 27), though the most significant SNP only explained 0.2% of the genetic variance. None of the SNP reported by de Hass et al. (2011) were corroborated in Pickering et al. (2015), despite both studies using the same methane prediction equation on Holstein cattle. Instead, Pickering et

al. (2015) found one SNP on chromosome 7 was repeatedly associated with predicted methane over the course of a lactation period. Genome-wide association studies (GWAS) with predicted methane trait evaluation has not been extensively conducted in beef cattle; however, Uemoto et al. (2020a) did perform a GWAS with two predicted methane traits in Japanese Black cattle. The authors did not detect significant SNP associated with either trait. It should be noted that Uemoto et al. (2020a) used a different prediction equation than de Haas et al. (2011) and Pickering et al. (2015). Regardless of methane prediction equation selected, the QTL associated with predicted methane production traits remain unclear.

In order for selection of animals with low methane production to be possible, a large number of animals must be phenotyped. There are several techniques to phenotype animals for methane production, such as respiration chambers and portable emission measuring units (reviewed in Garnsworthy et al., 2019). However, it can be costly and time-consuming to obtain direct methane production measurements, especially on the number of animals needed to create a reliable reference population for genetic selection. Instead, it is more efficient to select on an indicator trait such as predicted methane production, or to utilize these indicator traits to bolster genetic prediction while large numbers of animals with methane emissions data are phenotyped. Several equations which use variables that are simpler or more cost-effective to measure than direct methane production (e.g., dry matter intake) have been formulated to estimate these values (Ellis et al., 2007; IPCC, 2019, Mills et al., 2003).

The objectives of this study were to evaluate the genetic correlations between different methane prediction models, calculate the heritabilities of these predicted methane prediction traits, and identify quantitative trait loci for each trait.

Materials and Methods

Study Design and Data Collection

Full details on animals and study design are described in Ahlberg et al. (2019). Briefly, feed intake information was obtained on 830 crossbred steers from May 2014 to May 2018 at the Willard Sparks feedlot at Oklahoma State University. All animal procedures were approved by the Institutional Animal Care and Use Committee at Oklahoma State University (protocol AG13-18) in accordance with Federation of Animal Science Societies (FASS, 2010) guidelines. Steers were fed in seven groups with two feeding protocols. Three groups were fed using a slick bunk protocol (group 1, n = 119; group 2, n = 115; group 3, n = 120) and four groups had ad libitum access to feed (group 4, n = 105; group 5, n = 123; group 6, n = 126; group 7 n = 122). Within group, steers were blocked by weight (heavy and light) then randomly assigned to one of four pens. Each pen held approximately 30 animals. Each steer was implanted with Compudose (Elanco Animal Health, Greenfield, IN), an implant containing estradiol 17ß (E2 ß), per facility protocol.

While on test, each group received a mixed ration of approximately 15% cracked corn, 51.36% wet corn sweet bran, 28.44% prairie hay, and 5.20% mineral supplement. The rations were analyzed by Dairy One, Inc. (Ithaca, New York) for percent dry matter and gross energy estimates. The quality of ingredients differed slightly for each group which led to variations in the gross energy values. The gross energy of the diet was 18.99, 19.40, 18.26, 18.89, 18.82, 18.68, and 18.91 megajoule (MJ) per kilogram dry matter (DM) for groups 1 through 7, respectively.

All animals were allowed a 21-d acclimation period followed by a 70-d feed intake trial period as outlined in the Beef Improvement Federation guidelines (BIF, 2016). Feed intake was

measured using an Insentec system (Hokofarm Group, Netherlands). The system consisted of 6 feed bunks and 1 water bunk placed under shade in each pen. Body weights were measured every 14 d during the 70-d trial period.

Phenotypes were filtered using the procedures outlined in Allwardt et al. (2017). Briefly, start and end weights were filtered based on bunk volume and system settings. Body weight was filtered for appropriateness by assuming that animals could gain or lose a maximum of 50 kilograms between weighing days. Methane traits were only calculated for animals with average daily feed intake that passed these quality control filters.

Phenotypes

Average daily gain (ADG) was found by regressing time on the body weight measurements of each animal to account for differences in rumen fill. Mid-test body weight was calculated for each steer by multiplying each animal's ADG by 35 then adding the intercept from the regression analysis.

Methane emissions were predicted for each animal using three different methane prediction models. All models selected for use in this study were chosen for a multitude of reasons: 1) all utilize feed intake in some way, a trait that was consistently measured across groups, 2) all have performed well when evaluated against observed methane datasets (Ellis et al., 2007; Ellis et al., 2009; Kebreab et al., 2008), and 3) all are commonly used throughout methane prediction literature (de Haas et al. 2011, Pickering et al., 2015, Hayes et al., 2016). The first methane prediction trait was predicted using the model outlined in Ellis (Ellis et al., 2007) and detailed here:

$$EMP_i = \frac{[3.272 \ + (\ 0.736 * DMI_i)\ ]}{0.05565}$$

where EMP_i is the average daily methane emission of animal *i* in grams from the Ellis et al. (2007) equation and DMI_i is average daily dry matter intake of animal *i* in kilograms. Ellis et al. (2007) used a dataset of observed methane measurements from 172 trials (83 beef and 89 dairy) to create 32 original methane prediction equations. Of those 32 equations, 14 were trained on the beef data, 8 were trained the on dairy data, and 10 were trained on the combined data. The authors then tested the 32 methane prediction equations against each other and several extant equations to determine which model was the most accurate for each dataset. This equation had the lowest error of all the equations when evaluating the combined dataset (Ellis et al., 2007). It was chosen for inclusion because the diet formulation of the steers in this study, a major factor in methane production, most closely aligned with the average diet composition in the combined dataset of Ellis et al. (2007).

Second, methane production was predicted with the first nonlinear equation from Mills et al. (2003) as follows:

$$MMP_i = \frac{56.27 - (56.27 * e^{-0.028 * DMI_i})}{0.05565}$$

where MMP_i is the average daily methane emission of animal *i* in grams from the Mills et al. (2003) equation and DMI_i is average daily dry matter intake of animal *i* in kilograms. Most methane equations are linear regressions (Ellis et al., 2007), and thus as the predictor variable (often DMI) continues to increase as the predicted methane production continues to increase. However, Mills et al. (2003) reasoned that a nonlinear, diminishing returns relationship between intake and methane production may be more biologically appropriate. This equation was chosen to be included in this study due to its nonlinear nature. It is worth noting that Mills et al. (2003) trained and evaluated this model on a dairy cattle dataset, and it was not tested in beef cattle data.

By applying it to a beef dataset as in this study, it is assumed that there are no differences in rate of methane production between beef and dairy animals.

Finally, methane production was also predicted using the IPCC Tier 2 (IPCC, 2019) equations as follows:

$$IMP_{ij} = \frac{GE_j * \left(\frac{6.3}{100}\right) * DMI_i}{0.05565}$$

where IMP_{ij} is the average daily methane emission in grams of animal *i* consuming ration *j* as calculated by the IPCC (2019) equation, GE is the gross energy of ration *j* in MJ per kilogram, DMI_i is the average daily dry matter intake of animal *i*. The International Panel on Climate Change (IPCC) is the intergovernmental body tasked with assessing the science concerning anthropogenic climate change, of which ruminant emissions are a part. The IPCC has created three models used for estimating enteric methane production. Tier 2 (IPCC, 2019) was chosen for this study as it is more accurate than Tier 1 while Tier 3 required input variables not gathered during the course of the trial.

Genotypes

Two tubes per animal containing 8.5 milliliters of blood were drawn on days when weights were collected during the feeding period in vacutainer tubes containing 1.5 mL of the anticoagulant citrate dextrose. Samples of DNA were extracted using a phenol:chloroform:isoamyl alcohol extraction and ethanol precipitation. The DNA samples were sent to GeneSeek (Lincoln, NE) for genotyping on the GeneSeek Genomic Profiler genotyping array (GGP 150K). Thresholds for quality control were set so that that SNP with minor allele frequency less than 0.05 and SNP and animals with call rates less than 0.90 were removed from the analysis. After quality control, 782 animals and 124,100 SNP were used in the analysis.

Statistical Analysis

For statistical analysis, data from all groups was included. All analyses were performed with R (R Core Team, 2020), with the exception of the genetic evaluation. The minimum, mean, maximum, standard deviation for each trait, and Pearson and Spearman correlations between the traits were calculated with the "stats" package in R (R Core Team, 2020). The "stats" package in R (R Core Team, 2020) was also used to determine differences ($P < 0.05$) between the trait means with a two-tailed t-test.

Genetic analyses were conducted using genomic best linear unbiased prediction (GBLUP) methodology (Aguilar et al., 2010; Christensen and Lund 2010) where all relationships were defined solely using genomic data. Genetic relationships were determined using the genomic relationship matrix technique described in VanRaden (2008) and constructed as follows:

$$\boldsymbol{G} = \frac{\boldsymbol{Z}\boldsymbol{Z}'}{2\sum p_i(1-p_i)}$$

where **G** is the genomic relationship matrix and **Z** is a matrix generated by subtracting **P** (allele frequencies, p_i, expressed as a difference from 0.5) from **M** (a matrix of markers each individual inherited).

The three predicted methane traits would not converge in a multivariate model because of the extremely high correlations between them. Therefore, variance components and heritabilities for each trait were estimated using an average information restricted maximum likelihood (AIREML) algorithm in the BLUPF90 software package (Misztal *et al*., 2014) using the following univariate animal model:

$$[\boldsymbol{y}_i] = [\boldsymbol{X}_i\boldsymbol{b}_i] + [\boldsymbol{Z}_i\boldsymbol{u}_i] + [\boldsymbol{e}_i]$$

where **y** is a vector of phenotypes for trait *i*, **b** is a vector of fixed effects (group) and covariates (midtest weight) for trait *i*, **X** is an incidence matrix relating phenotypes to the fixed effects and covariates in **b** for trait *i*, **u** is a vector of additive direct genetic effects for trait *i*, **Z** is an incidence matrix relating phenotypes to the additive direct genetic effects in **u** for trait *i*, and **e** is a vector of random residuals for trait *i*. All the predicted methane equations chosen for this study are functions of feed intake (DMI or gross energy intake). Body weight and DMI have a strong, positive correlation (Martin et al., 1955). Therefore, to account for differences in predicted methane production caused by differences in body weight, mid-test weight was added as a covariate to the animal model.

The univariate animal model was used to calculate each animal's estimated breeding value (EBV) and standard error of prediction for each trait utilizing the BLUPF90 suite of programs. The standard error of prediction for each animal for each trait was squared to calculate the prediction error variance. The prediction error variance for each EBV was then used to estimate the accuracy of the EBV in R (R Core Team, 2020). The following accuracy equation defined in the Beef Improvement Federation Guidelines (BIF, 2020) was used:

$$Accuracy_{BIF} = 1 - \left(\sqrt{\frac{prediction\ error\ variance}{additive\ genetic\ variance}} \right)$$

Further, classical animal breeder accuracy was also calculated using the following conversion equation from the Beef Improvement Federation Guidelines (BIF, 2020):

$$r_{EBV,BV} = \sqrt{1 - (1 - Accuracy_{BIF})^2}$$

where $r_{EBV,BV}$ is the correlation between the estimated breeding value and the true breeding value. Pearson and Spearman correlations between the EBV for each trait were calculated using the "stats" R (R Core Team, 2020).

A GWAS was conducted for each trait using the postGSf90 function in the BLUPF90 suite of programs (Misztal et al., 2014) in combination with the univariate animal model employed for the variance component estimation and EBV calculations. The P-values of each SNP were matched to the ARS 1.2 SNP map provided by Neogen (Lincoln, NE) for the GGP 150k genotyping chip. Manhattan plots were then created using the qqman package in R (Turner, 2018). The cattle ARS 1.2 assembly (Rosen et al., 2020) was used in combination with JBrowse (Buels et al., 2016) to search for possible candidate genes. Candidate genes were determined to be any genes with functions possibly related to predicted methane production within 250 kilobases upstream or downstream of the SNP of interest. A range of 250 kilobases was chosen to account for moderate linkage disequilibrium (McKay et al., 2007). The UniProt Consortium database (2021) was used to investigate functionality of candidate genes. In addition, the cattle QTL database (Hu et al., 2019) was used to determine if any SNP close to the significance threshold in this study have also been associated with other traits in previous literature

Results and Discussion

Summary Statistics

The summary statistics for each methane production trait are listed in Table 2.1. All traits had significantly different means ($P < 0.001$). This has been observed in previous literature as Ellis et al. (2007), Ellis et al. (2009), and van Lingen et al. (2019) have all reported differences in predicted methane estimates when applying multiple prediction models to the same dataset. The standard deviation for EMP was much lower than that of the other two traits. This is because the prediction models are formulated in such way that the change in grams of methane resulting from a one-unit change in DMI for the equation from Ellis et al. (2007) was less than the rate of change from the other equations until the equation from Mills et al. (2003) reaches 28 kilograms

of DMI. In other words, the difference in methane production between an animal with a DMI of 10 kilograms and an animal with a DMI of 11 kilograms is not as great for the Ellis et al. (2007) equation as it was for the other equations. This formulation restrained the predicted methane production of the animals in this dataset to a narrower margin, and consequently a smaller standard deviation, than the other two equations. As previously stated, the equation from Mills et al. (2003) was chosen for inclusion because a nonlinear association between methane production and intake was thought to be more biologically appropriate as it would be unlikely for methane production to continue to increase at the same rate as DMI increases. In short, the Mill et al. (2003) equation was intended to limit the maximum methane predicted. Therefore, it is interesting to note that MMP had the greatest mean and maximum of all the traits. The aforementioned relative rate of increase in predicted methane from one additional unit of DMI at the levels of DMI seen in this data is much greater for the Mills et al. (2003) equation compared the equations detailed by Ellis et al. (2007) and IPCC (2019). Further, the Mills et al. (2003) equation was trained on feed intake observations in mature dairy cattle. The coefficients detailed in the model may have been accurate for the high DMI observed in dairy cattle, but the model may not perform as well when data from lower intake beef animals. This relatively poor performance was demonstrated by the Mills et al. (2003) model's high root mean square prediction error when attempting to predict the observed methane production of a beef dataset (Ellis et al., 2007).

The Pearson phenotypic correlations between all three traits were above 0.99 because each trait was derived from feed intake (Table 2.2). The high Pearson correlations indicate the values themselves behaved similarly, even though the actual predicted methane measurements differed.

The Spearman correlation for EMP and MMP was 1, indicating these traits ranked animals the exactly the same. The Spearman correlations between EMP and IMP and between IMP and MMP were also very high at 0.99. High Spearman coefficients indicate the animals' phenotypes ranked similarly regardless of trait.

Heritability

The genetic variance estimates for each trait are reported in Table 2.3. The heritabilities were 0.71 ± 0.11, 0.74 ± 0.11, and 0.70 ± 0.11 for EMP, MMP, and IMP, respectively. In comparison, Brito et al. (2018) estimated the heritability of predicted methane in cattle to be 0.26 ± 0.02. Brito et al. (2018) performed a meta-analysis of methane heritability estimates from 18 studies. Of those 18 studies, however, only 8 used a prediction method to obtain methane phenotypes. Further, the majority of the 8 predicted methane studies were conducted in dairy cattle. Of all the literature compiled by Brito et al. (2018), only one study reported the heritability of predicted methane in beef cattle, Sobrinho et al. (2015). The authors of Sobrinho et al. (2015) used three different equations to estimate predicted methane for 955 Nellore cattle. None of the equations overlapped between and this study and Sobrinho et al. (2015), however, body weight was also fitted as a covariate in the genetic analysis for both. The heritability of predicted methane was 0.32 ± 0.07, for all three prediction models used. Another study that estimated the heritability of predicted methane traits in beef cattle was Uetmoto et al. (2020a). The authors of Uemoto et al. (2020a) utilized two methane prediction equations. One was developed by Uemoto et al. (2020b) for cattle on high concentrate diets and the other from Shibata et al. (1993) which has been adopted for national greenhouse gas evaluations in Japan. Uemoto et al. (2020a) calculated heritabilities of 0.54 ± 0.05 of 0.56 ± 0.05 for predicted methane emission of Japanese Black steers using the equations of Uemoto et al. (2020b) and

Shibata et al. (1993), respectively. The heritabilities reported for predicted methane traits in this study are greater than the heritabilities reported for predicted methane traits in Brito et al. (2018), Sobrinho et al. (2015), or Uemoto et al. (2020a).

Alternatively, the traits presented in this study can be viewed as functions of average daily DMI in a population of growing animals. From that perspective, herititablies of 0.71 ± 0.11, 0.74 ± 0.11, and 0.70 ± 0.11 are within literature estimates. For example, Ahlberg et al. (2019), reported the heritability of DMI to be 0.67 (± 0.04). This is especially pertinent since the animals in Ahlberg et al. (2019) had substantial overlap with the animals analyzed in this study (578 animals in common with an addition 252 animals in this study). Further, Koch et al. (1963) and Archer et al. (1997) estimated the heritability of DMI for cohorts of Angus, Hereford, and Shorthorn growing animals to be 0.64 (± 0.12) and 0.62 (± 0.12), respectively. More recently, Freetly et al. (2020) calculated 0.82 (± 0.12) as the heritability of for average daily dry matter in growing heifers.

Estimated Breeding Values

Estimated breeding values were generated for each steer and each trait (Table 2.4). As expected, the mean EBV for each trait was approximately zero. Generally, these estimates follow the same pattern as the summary statistics for the phenotypic traits. Ellis methane production has the smallest range of values and the correspondingly lowest standard deviation. Curiously, while both MMP and IMP had a greater range than EMP, IMP had a greater standard deviation, where the standard deviations for EMP and MMP were relatively similar. The difference may lie in the fact that IMP has a slightly larger phenotypic range than MMP or perhaps it is because the IPCC et al. (2019) methane prediction equation was different for each group due to the inclusion of the

group-specific GE for the ration. This latter hypothesis would be supported by the relatively large residual variance of IMP as seen in Table 2.3.

Similar to the phenotypes of the traits, the EBV all share a very high Spearman correlation of 0.99. This supports the premise that any of the predicted methane traits described in this study could be utilized for selection and the animals would rank almost exactly the same.

When discussing the accuracy, it is important to remember the accuracy is not how accurate the models used were in predicting actual methane production of the animals. Instead, accuracy is defined here as the correlation between the EBV and the true breeding value of any given individual. The BIF accuracies for each trait are lower than the conventional accuracies because the BIF Guidelines (2020) utilize a more conservative estimate. Nonetheless, even with the more stringent calculation, the BIF accuracies for the EMP, MMP, and IMP are moderately high. In addition, the conventional breeder's accuracies are very high. The high accuracies of this traits are to be expected due to the correspondingly high heritability estimates because the higher the heritability, the more an individual's own phenotype can be relied on as an indicator for that individual's true breeding value. In fact, the mean accuracy for IMP and MMP are slightly larger than the square root of the heritability estimates for those traits, as would be expected when some of the animals had relatives with phenotypes in the data.

Selection

The predicted methane production traits examined in this study and in other literature have been shown to have genetic variation between animals (Table 2.3, de Hass et al., 2011, Pickering et al., 2015), therefore reducing predicted methane production via selection is possible. The high heritabilities of the three methane prediction traits (0.70 - 0.74) indicate genetic progress could be made relatively quickly because an animal's own phenotype would be a good

indicator of its offsprings' phenotype. Further, any of the three traits examined would be equally effective because the Spearman correlations of the EBV for each trait were 0.99. Nonetheless, in a national genetic evaluation, the ideal setup would be for each animal to have predicted methane production estimated from the same equation. From the equations presented here, the Ellis et al. (2007) equation would likely be the best choice for a national beef evaluation because it would be the most robust to animals fed varying diets. In addition, the GWAS demonstrates that all the methane prediction traits are associated with the same genetic loci and candidate genes.

There are drawbacks to selecting on predicted methane traits due to their high correlations with DMI, body weight, and gain. Any direct selection to decrease predicted methane traits would also decrease those associated traits. Therefore, it would be most advantageous to account for those correlations by including predicted methane production in a properly weighted selection index with DMI, body weight, and gain. Not only would a selection index account for the correlations between predicted methane production and economically important traits, but it would also give a weight to predicted methane production to ensure it was not over-emphasized.

SNP Effects

Observed methane has been shown to have high phenotypic (0.71 ± 0.02) and genetic (0.84 ± 0.06) correlations with DMI (Donoghue et al., 2016). The correlation between DMI and predicted methane production, often a function of DMI, are even higher. Pickering et al. (2015) and de Haas et al. (2011) reported a phenotypic correlation of 0.99 for DMI and predicted methane while Pickering et al. (2015) and Uemoto (2020a) both reported 0.999 genetic correlation between the two traits. The Pearson correlations between average daily DMI and each predicted methane trait used in this analysis ranged from 0.99 to 1. Therefore, it is important to

understand whether any significant SNP association found for predicted methane traits are also significant for DMI.

The threshold for significance for SNP was set at 5 on a $-\log_{10}$ P-value scale. As shown in Figures 2.1 to 2.3, no SNP exceeded this threshold, likely because of the small sample size. Interestingly, IMP and MMP resulted in SNP much closer to the significance threshold than EMP. Table 2.5 details the 25 SNP closest to the significance threshold for each trait. Both IMP and IMP had the same top 25 SNP, while MMP identified rs110629540 on *Bos taurus* autosome (BTA) 9 rather than rs110629540 on BTA 14.

Two SNP close to the threshold for significance in all traits have been associated with other traits in previous literature. One SNP on BTA 3, rs110220315, was significantly associated with vitamin D intake in beef cattle by Casas et al. (2013). The authors reported rs110220315 to be within 10,000 bases of *CYP2J2*, a gene related to the bioactivation of vitamin D. However, the authors of Casas et al. (2013) utilized the University of Maryland version 3 assembly which placed rs110220315 approximately 600,000 bases downstream of its ARS 1.2 assembly locus. The difference in location for rs110220315 between the assemblies used by Casas et al. (2013) and this study makes it difficult to determine if there is a relationship between vitamin D intake and predicted methane production. The other SNP previously identified in literature is rs133609351 on BTA 20. This SNP was associated with milk yield, milk fat percentage, and milk protein percentage by Jiang et al. (2019). However, Jiang et al (2019) employed the UMD 3.1 cattle genome assembly which positioned rs133609351 nearly 23,000 bases upstream of the locus reported in the ARS 1.2 assembly. Nonetheless, a 23,000 base pair range still falls within the range of LD (McKay, 2007) and milk yield, like predicted methane production, is heavily driven by DMI (Brown et al., 1977).

In addition, three SNP in the top 25 SNP for all three methane prediction traits, were located within 250 kilobases of other loci that had been previously associated with other traits. One such SNP was rs109043582 on BTA 3, which is located in the same gene (*DAB1*) as two SNP associated with rump width by Cole et al. (2011) and another associated with metabolic body weight by Seabury et al. (2017). Both rump width and metabolic body weight may be related to predicted methane as larger animals tend to eat more and are therefore expected to produce more methane than smaller animals. Similarly, rs41652941 on BTA 4 was near two SNP associated with body weight gain (Snelling et al., 2010). In addition, rs134083327 on BTA 12 was also in close proximity to a SNP identified by Seabury et al. (2017) as associated with ADG. Body weight and ADG are both highly correlated with DMI and, as a function of DMI, predicted methane production.

There were 14 candidate genes identified for each trait because several top SNP clustered around the same candidate gene or were in a region with no identified genes. It is worth noting that of the 14 candidate genes for EMP and IMP, 13 were also candidate genes for MMP. Generally, most candidate genes shared between all three traits can be grouped by functionality. The largest functional group were related to collagen. For example, *COL1A1*, *DCN*, and *P4HA2* are a component of collagen, bind collagen, and play a role in collagen fibril organization, respectively (The UniProt Consortium, 2021). Collagen is connective tissue and the most abundant protein in animals (Shoulders and Raines, 2009). High turnover rate of collagen has been linked with accelerated growth rate in cattle (Wu et al., 1981) and lambs (Sylvestre et al., 2002). Feed intake (DMI) shares a strong phenotypic (0.60) and genetic (0.87 ± 0.09) correlation with growth (ADG) (Nkrumah, et al., 2007). Further, predicted methane traits are functions of

DMI; therefore, animals with genetic variants enabling high collagen turnover may exhibit accelerated growth and a subsequentially greater DMI.

Another group of candidate genes with similar function were associated with microtubules. Both *HOOK1* and *DAB1* are linked to microtubule binding, while *KIF13A* depends on microtubules for intracellular transport. Microtubules provide structure to the cytoskeleton and differences in genes controlling their arrangement may imply differences in cell energy efficiency. Two other functional groups were apparent, one concerned with ubiquitin ligase (*FBXO4, FBXO5,* and *MARCH3)* and the other linked to regulating the binding of RNA polymerase II for DNA transcription (*ELK3* and *ZNF93*). The function of each of these groups is very broad making it difficult to determine their specific potential role in predicted methane production. Ubiquitin is involved in post-translational modifications of several different proteins while all DNA that expresses proteins needs to be transcribed (The UniProt Consortium, 2021). Interestingly, *ELK3* was identified as a possible regulator for genes related to feed conversion ratio and feed efficiency ratio traits in de Lima et al. (2020).

There were a few candidate genes that did not fall into any general group. For example, *TRIL* is related to immunity and inflammation (The UniProt Consortium, 2021) which is not uncommon as genes related to the immune system have been previously associated with divergent weight gain and feed intake (Lindholm-Perry et al., 2016a-b). Curiously though, *TRIL* in has also been suggested to have a role in leptin sensitivity (Moura-Assis et al., in press). The inhibition of *TRIL* in certain neurons may lead to a reduction of inflammation in the hypothalamus, which, in turn, may also lead to an increased sensitivity to hypothalamic leptin. Because leptin is a hormone related to feed intake (Nkrumah et al., 2004), it is possible that a slight increase in *TRIL* may lead to reduced leptin sensitivity and increased feed intake. Another

gene close to significance for all three traits, *DDC*, is involved in the transformation of L-dopa to the hormone dopamine (The UniProt Consortium, 2021). The connection between *DDC* and predicted methane production is unclear; however, it was suggested to be differentially expressed in low and high residual feed intake animals, along with *COL1A1* and *KIF21A* (related to *KIF13A*) by Chen et al. (2011). One SNP (rs43076526 on BTA7) was the closet to significance for all predicted methane traits and had two potential candidate genes nearby. The first, *MARCH3*, has already been discussed while the second was *ALDH7A1*. The latter gene produces a protein that protects the cell from oxidative stress (The UniProt Consortium, 2021). Moreover, *ALDH7A1* may also be linked to collagen turnover because oxidative stress may decrease collagen synthesis in some muscle groups (Archile-Contreras and Purslow, 2011). Thus far, all candidate genes discussed have been shared by all three traits, however, *GDF6* was only in the top 25 SNP of IMP. This gene is involved in the formation of the skeleton (The UniProt Consortium, 2021) and was suggested as a candidate gene for ADG, weight, and other growth parameters by Zhang et al. (2018).

Conclusion

All three predicted methane traits, as determined by equations from Ellis et al. (2007), Mills et al. (2003), and IPCC (2019), produced similar estimates of methane production. All three traits demonstrated genetic variation, which indicates genetic selection on predicted methane production is possible. Moreover, all predicted methane traits had a heritabilities ranging from 0.70 to 0.74, suggesting genetic progress could be made relatively quickly. None of the 124,100 SNP investigated reached the threshold for significance; however, the 25 SNP closest to that threshold were investigated and found to be very similar between all three traits. Candidate genes 250 kilobases upstream or downstream of those SNP were identified and

assessed for functionality. Several candidate genes grouped together in a functional group related to collagen. Prior literature suggests collagen turnover is related to growth rate and feed intake. Given the predicted methane traits used in this study are functions of feed intake, the relationship between predicted methane production and collagen warrants further investigation.

Figure 2.1

Manhattan plot showing result of genome-wide association mapping for methane production predicted by Ellis et al., 2007

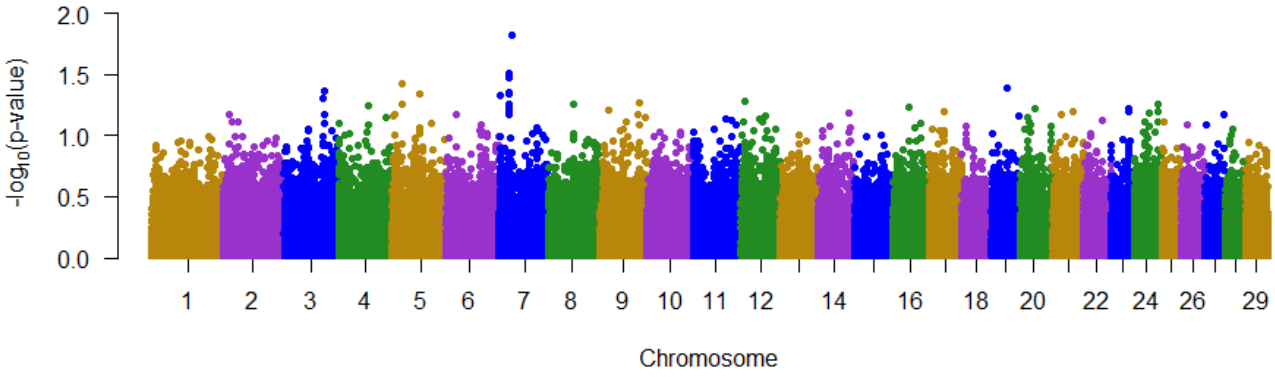


Figure 2.2

Manhattan plot showing result of genome-wide association mapping for methane production predicted by Mills et al., 2003 with a significance threshold of 5.0

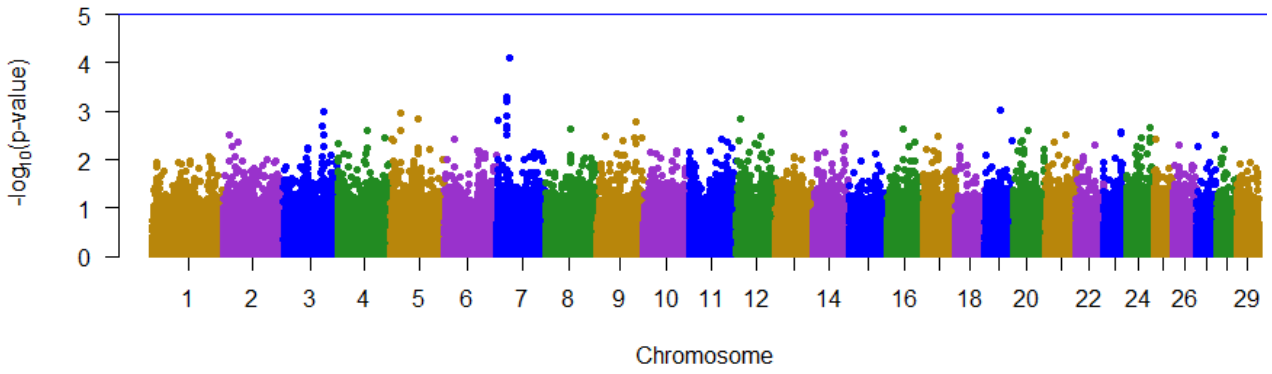


Figure 2.3

Manhattan plot showing result of genome-wide association mapping for methane production predicted by IPCC, 2019 with a significance threshold of 5.0

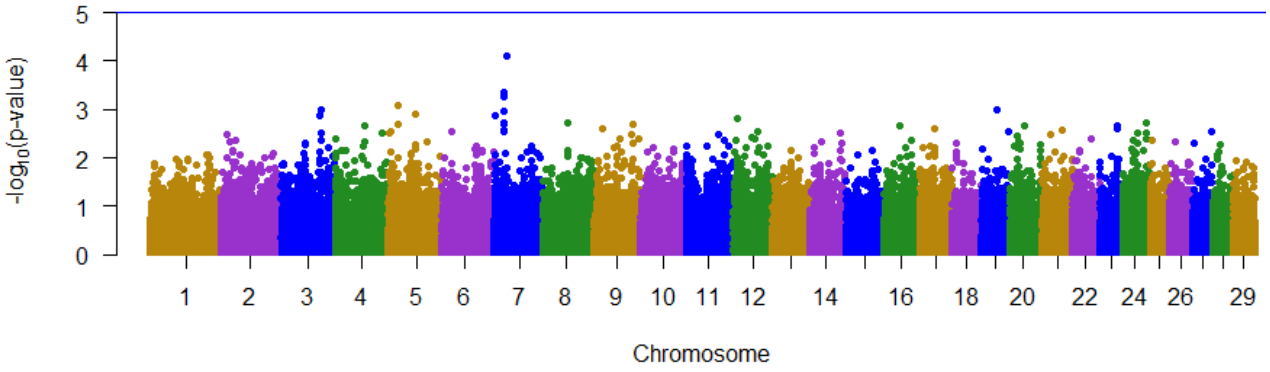


Table 2.1

Summary statistics of average daily methane production (g methane/d) for each methane estimation equation

	Mean	Minimum	Maximum	Standard Deviation
EMP	200.9[a]	138.2	272.7	19.7
MMP	261.8[b]	156.4	368.2	31.3
IMP	229.0c	131.8	344.5	32.0

Means with different superscripts are statistically different
EMP is methane predicted using an equation adapted from Ellis et al. (2007)
MMP is methane predicted using an equation adapted from Mills et al. (2003)
IMP is methane predicted using an equation adapted from IPCC (2019)

Table 2.2

Phenotypic correlations (Pearson above the diagonal, Spearman below the diagonal) between methane prediction traits

	EMP	**MMP**	**IMP**
EMP		0.99*	0.99*
MMP	1*		0.99*
IMP	0.99*	0.99*	

*P < 0.01

EMP is methane predicted using an equation adapted from Ellis et al. (2007)
MMP is methane predicted using an equation adapted from Mills et al. (2003)
IMP is methane predicted using an equation adapted from IPCC (2019)

Table 2.3

Variance components (standard errors) for each predicted methane trait

	Genetic Variance	Residual Variance	Heritability
EMP	150.57 (27.0)	62.4 (21.9)	0.71 (0.11)
MMP	401.4 (69.2)	143.8 (55.6)	0.74 (0.11)
IMP	390.9 (71.0)	165.1 (57.5)	0.70 (0.11)

EMP is methane predicted using an equation adapted from Ellis et al. (2007)
MMP is methane predicted using an equation adapted from Mills et al. (2003)
IMP is methane predicted using an equation adapted from IPCC (2019)

Table 2.4

Summary statistics and accuracies of estimated breeding values for average daily methane production (g methane/d) for each methane estimation equation

	Mean	Minimum	Maximum	Standard Deviation	BIF accuracy	Classical Animal Breeding Accuracy
EMP	0.003	-38.7	30.8	11.0	0.46	0.84
MMP	-0.01	-48.8	34.8	13.5	0.51	0.87
IMP	0.004	-63.9	50.4	17.7	0.46	0.84

EMP is methane predicted using an equation adapted from Ellis et al. (2007)
MMP is methane predicted using an equation adapted from Mills et al. (2003)
IMP is methane predicted using an equation adapted from IPCC (2019)

Table 2.5

Single nucleotide polymorphisms (SNP) most closely associated with predicted methane production traits

SNP ID	Chromosome: Position	$-\log_{10}$ P-value	Candidate Gene	Candidate Gene Function
rs110220315	3: 86090597	1.31	*HOOK1*	Microtubule binding
rs110058749	3: 88164394	1.37	*DAB1*	Microtubule binding
rs41652941	4: 67207224	1.24	*TRIL*	Lipopolysaccharide binding
rs110309656	5: 21475995	1.26	*DCN*	Collagen binding
rs109244569	5: 21516232	1.42	*DCN*	Collagen binding
rs137645685	5: 60495101	1.34	*ELK3*	DNA-binding transcription factor activity, RNA polymerase II specific
rs43497423	7: 3522788	1.33	*ZNF93*	DNA-binding transcription factor activity, RNA polymerase II specific
rs43508672	7: 22191462	1.24	*P4HA2*	Collagen fibril organization
rs43508669	7: 22195580	1.24	*P4HA2*	Collagen fibril organization
rs43508667	7: 22197623	1.48	*P4HA2*	Collagen fibril organization
rs29023390	7: 22202959	1.35	*P4HA2*	Collagen fibril organization
rs43508661	7: 22204260	1.25	*P4HA2*	Collagen fibril organization
rs43141114	7: 22268814	1.35	*P4HA2*	Collagen fibril organization
rs43509246	7: 22328341	1.51	*P4HA2*	Collagen fibril organization
rs43076526*	7: 27252564	1.82	*MARCH3*	E3 ubiquitin protein ligase
			ALDH7A1	Oxidoreductase
rs41621748	8: 56479469	1.25	*No identified genes*	
rs109044910	9: 18387990	1.21	*LOC 101903114*	Non-coding RNA
rs43605790‡	9: 89807465	1.27	*FBXO5*	Negative regulation of ubiquitin

				protein ligase; Microtubule polymerization
rs134083327	12: 10040464	1.28	*No identified genes*	
rs110629540¶	14: 68002844	2.56	*GDF6*	Skeletal formation
rs110393484	16: 37286950	1.23	*F5*	Blood coagulation
rs134127572	19: 36424186	1.39	*COL1A1*	Component of group I collagen
rs133609351	20: 32437127	1.23	*FBXO4*	Substrate recognition component of SCF ubiquitin protein ligase complex
rs133044483	23: 39502283	1.22	*KIF13A*	Microtubule dependent intracellular transport
rs136158794	23: 39522823	1.2	*KIF13A*	Microtubule dependent intracellular transport
rs133940625	24: 53068328	1.26	*DDC*	L-dopa decarboxylase activity

*Multiple candidate genes
‡SNP in top 25 for Ellis predicted methane and IPCC predicted methane only
¶SNP in the top 25 for Mills predicted methane only
Possible candidate genes within 250 kilobases of the SNP
Candidate gene functions according to The UniProt Consortium.

Chapter 3 - Environmental Sustainability of Simulated Cow-Calf Operations in the Great Plains

Abstract

Environmental sustainability is a key component to overall sustainability of the beef industry. Simulation provides the opportunity to assess the environmental impact of current practices and evaluate the outcomes of alternative strategies. The objective of this project was to use a stochastic model to simulate a 100 head cow-calf operation to determine land, water, and fertilizer requirements as well as methane emissions for various regional beef production scenarios. The simulations were parameterized to replicate 74 different land regions in the Great Plains and six varying genetic potentials for mature body weight and peak lactation for cattle within those regions for a total of 444 unique scenarios. Further, the resource inputs of diets including corn products were compared to diets including grain sorghum products in regions where grains are often fed by cow-calf producers. The average amount of land use for each herd was 711 hectares when corn products were used and 714 hectares when sorghum products were used. Corn-based diets required an average of 30,588,948 liters of blue water (irrigation and drinking water) per herd per year, while sorghum-based diets required an average of 42,776,720 liters per herd per year. There were negligible differences in fertilizer estimates between corn and sorghum-based diets (26,532 and 26,523 kilograms of nitrogen per hectare, respectively). The average enteric methane production for all scenarios was 8,898 and 8,925 kilograms per herd per year for corn and sorghum-based diets, respectively. In general, large, high lactation cattle had the largest environmental footprint, whereas small, low lactation cattle had the smallest. Depending on the variable evaluated, the impact of body size and lactation potential varied in importance. However, animals with a higher lactation potential required more land to

grow feedstuffs regardless of size. For total land, blue water, fertilizer, and enteric methane production, however, heavier animals had a larger environmental impact than lighter animals with the same lactation potential. Small, high lactation animals had the smallest environmental impact when natural resource use was scaled by kilograms of calf weaned.

Introduction

Sustainability in beef production has recently received a great deal of attention. Like all businesses, beef sustainability has three pillars: environmental, social, and economic. While all pillars are of equal importance, the environmental pillar has received the most scrutiny from the public. The most discussed aspect of the environmental pillar is the greenhouse gas (GHG) footprint of the beef industry; however, this pillar also encompasses the land, water, and fertilizer resources necessary for beef production. The technique for determining the environmental footprint of a product like beef, is known as a life cycle assessment (LCA). A LCA tracks the environment impact of a product from its manufacturing (including necessary inputs) through to its disposal.

Performing a LCA of beef in the United States is a difficult task. This is partly because the resources used and the GHGs emitted are difficult to track and accurately measure. Further compounding the problem is the large scale of the United States beef industry and the variety of management and environmental conditions. The USDA reports there are over 93 million beef cattle in the United States as of January 1, 2021 (USDA NASS, 2021), and all are being raised in a diverse array of climate and management scenarios. Thus, one of the most robust and effective methods available to the scientific community to investigate the environment footprint of the beef industry is simulation.

Simulation is the act of using real world data and a variety of statistical models to predict or recreate the outcome of a system. For environmental sustainability of beef, this means using the real- world practices of beef cattle producers, coupled with natural phenomena like weather and the approximated nutrient requirements of cattle, their emissions, and the natural resources required in their upkeep.

One of the first major studies to use a fully self-contained model was Rotz et al. (2013). Here the authors developed a tool, the Integrated Farm System Model (IFSM), to assess the environmental and economic sustainability of farming systems. The model was first applied to the Meat Animal Research Center (MARC), a facility with known feed and water use quantities and management practices, in order to determine accuracy of the predictions from the model. The model itself utilized crop production, weather, land resources, and cattle diets as inputs. In turn, the model simulated values for feed production, resource use, and GHG emissions. Over a 24-year simulation, the production system at MARC produced an average of 10.9 (± 0.6) kg carbon dioxide equivalent per kilogram of body weight sold per year. Further, this system required an annual 26.5 (± 4.5) MJ of fossil fuel energy and 2790 (± 910) liters of irrigation water per kilogram of body weight sold. When compared to the real-world data, all of the simulated data was within 1% of the reported numbers. These results show that not only can simulation data be more easily gathered than real-world data, but simulations can also be extremely accurate.

Before a simulation that captured the environmental impact of the beef industry could be created, data about real-world production practices needed to be gathered so the information input into the simulation would be accurate. Therefore, a series surveys were sent out to producers involved in all stages of raising beef (Asem-Hiablie, et al., 2015, Asem-Hiablie, et al.,

2016, Asem-Hiablie, et al., 2017, Asem-Hiablie, et al., 2018a, Asem-Hiablie, et al., 2018b). Each publication reported the results of the survey from a different area of the United States. These surveys queried information about the cattle themselves (body weight, number of head), management practices (stocking rate, cow-to-bull ratio), and resources used (land, time, and machinery required). These surveys were then followed up with a representative number of farm visits to corroborate the general information gathered.

All the survey information (Asem-Hiablie, et al., 2015, Asem-Hiablie, et al., 2016, Asem-Hiablie, et al., 2017, Asem-Hiablie, et al., 2018a, and Asem-Hiablie, et al., 2018b), along with other information like weather and soil type, were used as inputs in the simulation performed by Rotz et al. (2019). The IFSM was used for a farm-gate LCA, or a measurement of the environmental footprint of animals from birth until they leave the feedlot. That information was used in combination with packing, processing, distribution, retail, and consumption data to calculate a baseline measurement for environmental sustainability in the United States. The average annual GHG emission was found to be 243 (± 26) teragrams of carbon dioxide equivalent per kilogram of carcass weight. In addition, the average annual blue water consumption was 23.2 (± 3.5) teraliters per kilogram of carcass weight. Rotz et al. (2019) demonstrated the powerful ability of simulation. Without simulation, estimating GHG emission and water footprint across an area as large as the United States with any reliability would have been an unwieldy endeavor.

With the vast number of beef cattle and the variety of different management practices used across the US, the task of cataloging and calculating natural resources going into the beef production system and the resulting GHG emissions is a daunting task. Luckily, the system of beef production lends itself to simulation, and simulation has been proven to be an accurate way

to assess resource use in beef production. While simulation is used extensively in LCAs, it can also be utilized in a similar manner to answer targeted research questions, about the environmental impact of beef production as outlined below.

Materials and Methods

Simulation Model Details and Static Parameters

This study utilized a stochastic simulation model developed to simulate beef productions systems while accounting for the natural variation in production that occurs due to random change, management decisions, and environmental factors. A full description of the mechanics and assumptions of the cow-calf simulation model (CCSM) used can be found in in Aherin (2020). Briefly, a stochastic model was used to simulate the occurrences of incidences like birth, weaning, morbidity, and culling seen in real-world production systems. The model captures the variation and complex feedback structure inherent in a beef production system by drawing from a distribution of production outcomes (parameterized from literature estimates for these outcomes) and having the resulting most probable outcome for one or multiple events determine the distribution of outcomes for other events. For example, nutrition affects postpartum interval length, which in turn affects the chances of an individual animal being culled. Any number of years and iterations can be parameterized. For this study, a timeframe of 24 production years, modeled with data from1995 through 2018, and 25 iterations was set for each scenario. These parameters balanced run time with generating enough information to have a reasonable estimate for each scenario across a variety of conditions and outcomes.

While each simulation had several variable inputs capturing the specifics of each scenario, most of the model's assumptions remained static. The model begins by assuming each herd is a 100- head straightbred cow-calf operation comprised of Angus cattle. Each herd is

assumed to retain replacement heifers bred to purebred Angus bulls. Cows are exposed for breeding for 63 days each year, from May 1 to July 3. The model assumed that each herd is on pasture from May 1 to October 31. The model took genetic factors like body weight and lactation potential, as well as environmental factors like weather into account to estimate the net energy requirement of each animal each day. From May 1 to October 31, the model calculated how much forage was available for grazing and, using the net energy of the forage specified by the user, calculated how much forage each animal needed to consume every day to maintain a body condition score of 5. Each animal could eat up to 2.7% of their bodyweight per day. If the animal could not meet its needs on forage alone, it was assumed that the animal was supplemented until either its needs are met, or supplementation accounted for 20% of the animal's daily intake. If the animal still could not consume enough net energy, it resulted in a loss of body condition and the odds of pregnancy and staying in the herd decreased. From November 1 to April 31 of the following year, the animals were assumed to be delivered a daily ration of hay and supplement to meet their nutritional needs.

The model output a variety of information ranging from the birth date of each animal to cost of production. For the purposes of this study, the outputs of most interest were the dry matter weights of the forage, delivered ration, and supplementation diets of each year of each iteration of each scenario, in addition to the number of animals in each age class (replacement heifer, bred heifer, or mature cow) for each year in each iteration of each scenario.

Variable Inputs

The Great Plains is a large region in the Central United States that is host to a large population of beef cows. For the purposes of this study, the Great Plains is defined as North Dakota, South Dakota, Nebraska, Kansas, Oklahoma, and Texas. These six states constitute a

vast area of land with a variety of different climates, management practices, and resources; therefore, further subdivision was necessary. Major Land Resource Areas (MLRAs) are areas that a have distinct pattern of climate, soil, and natural resources (NRCS, 2006). These MLRAs are the basic land regions for each scenario. Within the Great Plains, as defined for this study, there are 74 MLRAs (Figure 1).

The CCSM used variables that changed as each scenario was parameterized. For this project, animal genetic potentials (body weight, lactation potential), management techniques (diet formulation, stocking rate, etc.), MLRAs, and environmental components (climate and forage resource composition) were altered to create 444 unique scenarios which were parameterized in the CCSM.

Animal and Stocking Rate Parameters

The inputs parameterizing the animals were drawn from studies that describe the management practices of beef producers in various regions and were the same studies that provided the inputs for Rotz et al. (2019) (e.g., Asem-Hiablie, et al., 2015, Asem-Hiablie, et al., 2016, Asem-Hiablie, et al., 2017, Asem-Hiablie, et al., 2018a, and Asem-Hiablie, et al., 2018b). The two papers used for this study detailed the Southern Plains (Asem-Hiablie et al., 2015) and the Northern Plains (Asem-Hiablie et al., 2016). Each study (Asem-Hiablie et al., 2015, Asem-Hiablie et al., 2016) separates the region of interest into East, Central, and West in order to capture the management differences which occur as precipitation and forage resources change. Each MLRA was assigned to one of the regions described in either Asem-Hiablie et al. (2015) or Asem-Hiablie et al. (2016) These regions are the North East, North Central, North West, South East, South Central, or South West, and grouping was based on the geographic location of the MLRA. As seen in Table 3.1, each region has a unique average cow body weight and stocking

rate which was used a baseline for each scenario (Asem-Hiablie et al., 2015, Asem- Hiablie et al., 2016). The average cow body weight for each region was designated moderate body weight for the MLRAs in that region. Likewise, the average stocking rate of each region became the stocking rate associated with moderate-sized cows in each MLRA. Using the average cow body weight in each region as a baseline, the mature body weight of large cows was one standard deviation greater than the mature body weight of the moderate cattle if standard deviation information was available or 45.5 kg greater if no standard deviation of body weight was reported (Asem-Hiablie et al., 2015, Asem- Hiablie et al., 2016). Similarly, the mature body weight of small cows was one standard deviation less than the mature body weight of the moderate cows if standard deviation information was available or 45.5 kg less if no standard deviation of body weight was reported (Asem-Hiablie et al., 2015: Asem- Hiablie et al., 2016). The stocking rates for the large and small cattle were found by dividing the new body weight by the body weight of the moderate cow and multiplying that ratio by the stocking rate of the moderate cow. The body weights and stocking rates of replacement heifers and bred heifers were also defined. Body weight was set at 58% of mature cow body weight for replacement heifers (Larson, 2007) and 85% of mature cow body weight for bred heifers (Jurgens et al., 2012). Stocking rate was set for replacement and bred heifers as described above. Peak lactation potential was set at 11 kg (high) or 8 kg (low) as these values were slightly higher than average and slightly lower than average peak lactation yields, respectively (NRC, 2016). All possible pairwise combinations of these size and lactation potential values were utilized, which provided a combination of six genetic potentials simulated within each MLRA environment.

Weaning weights for each genetic potential were estimated using a regression equation expressed mathematically below:

$$WW_1 = 246 + (0.1476 * (MW_i - 547.95))$$

where WW_1 is the intermediate weaning weight 246 is the national average weaning weight of calves from beef production operations with between 50 and 199 animals (USDA, 2020), 0.1476 is the change in kilograms of calf weaning weight per 1 kilogram change in mature cow bodyweight (Ziegler, 2020), MW is the average mature weight of the genetic potential *i*, and 547.95 is the average mature bodyweight of cattle in all scenarios.

The intermediate weaning weight was then adjusted for lactation potential using the equation below:

$$WW_2 = WW_1 + (6.6 * (LP_i - 9.8))$$

where WW_2 is the approximated weaning weight fully adjusted for maternal genetic potential, 6.6 is a regression coefficient drawn from King et al. (2020) which reported that adjusted-205 day weaning weight increases by 6.6 kilograms for every 1 kilogram increase in lactation potential, LP is the peak lactation in kilograms for lactation potential *i*, and 9.8 is the average peak lactation of Angus cattle (Fraga, et al., 2013) used to scale the lactation potentials.

Forage Parameters

Because cow-calf herds depend heavily on grazing forages for feedstuffs, the annual production and seasonal nutritional composition of the forages in each MLRA was calculated and is outlined in Table 3.2a-b.

The Natural Resource Conservation Service (NRCS) provided estimates of annual forage production for intensively managed pasture ground and extensively managed rangeland within each MLRA (NRCS, personal communication, 2021). The NRCS also provided the area of each type of grazing land within each MLRA (NRCS, personal communication, 2021). Total annual

forage yield for each MLRA was calculated as the annual forage yield of pasture and rangeland and weighted by the respective relative percent area in each MLRA.

It is important to note the CCSM only accepts the net energy maintenance and net energy gain estimates of forage as inputs, not specific forage types or diets. The user is required to calculate the composition of the forage resource and appropriately calibrate the net energy estimates. The net energy estimates for grazing land were determined by first obtaining plant community composition from each MLRA (EDIT, 2021). The forage community composition was then narrowed down to those grass or forb species whose yields contributed at least five percent of the total yield. Of those high-yield species, only species with literature estimates of chemical composition throughout several months were used to represent each MLRA (Appendix A.1). Because species were selected for inclusion based on the highest annual yield, the implied assumption is the forage species with largest annual production also made up the majority of the herd's grazing diet. The percent composition for each species in each type of grazing land for each MLRA was found by dividing the mean annual production of each species by the sum of the production for all representative species in that type of gazing land in that MLRA. It is important to note that this process was only for estimating forage energy content of each MLRA and had no bearing on determining total forage yield. Next, a database of acid detergent fiber (ADF), total digestible nutrients (TDN), and or net energy estimates of over 40 species of grasses was compiled from literature. It included monthly data for the months of May through October (when the cattle were assumed to be on pasture). Chemical compositions were estimated for months with missing data using existing information as a basis for extrapolation. For example, the average ADF of two adjacent months was used if the ADF for a month between them was missing. The TDN was estimated by this equation from Adams et al. (1995):

$$TDN_{ij} = 88.9 - (0.779 * ADF_{ij})$$

where TDN is percent total digestible nutrients of the *i*th forage species in the *j*th month and ADF is the acid detergent fiber of the *i*th forage species in the *j*th month. Net energy maintenance for each forage species for each month was calculated by the equation below (Lardy, 2018):

$$NEM_{ij} = ((TDN_{ij} * 0.01318) - 0.132) * 2.204$$

where NEM is net energy maintenance in megacalories per kilogram of dry matter for the *i*th forage species in the *j*th month and TDN is percent total digestible nutrients of the *i*th forage species in the *j*th month. In addition, the TDN values were used to estimate net energy gain using this equation from Lardy, 2018:

$$NEG_{ij} = ((TDN_{ij} * 0.01318) - 0.459) * 2.204$$

where NEg is net energy gain in megacalories per kilogram of dry matter for the *i*th forage species in the *j*th month and TDN is percent total digestible nutrients of the *i*th forage species in the *j*th month. Once net energy estimates for each species and month were established, those values were multiplied by the percent composition for each species to create the net energy estimates for pasture and for rangeland for each MLRA. The final net energy estimates for forage in each MLRA for the months of May through October were the sum of the net energy estimates for pasture and rangeland weighted by the percent of pasture and rangeland in each MLRA. The net energy estimates of forage for each MLRA for the months of November through April were set equal to the net energy estimate of October. This was because the cattle were assumed to be delivered feed from November through April and the forage net energy estimate for those months was arbitrary and not used by the model for any relevant output described herein.

Fed Diet Parameters

Cattle diets vary greatly depending on location and price. Therefore, each MLRA was assigned to one of six diet regions: North East, North West, Central East, Central West, South East, or South West. These regions had some overlap with those developed by Asem-Hiablie et al. (2015) and Asem-Hiablie et al. (2016) but were independent entities based on availability of forage production data. The MLRAs in the Eastern regions had predominately cool-season forages, while those in the Western regions had more warm-season forages. The North region consisted of those MLRAs with the majority of their land mass in either North Dakota or South Dakota. The Central region consisted of those MLRAs with the majority of their land mass in either Nebraska or Kansas. The South region consisted of those MLRAs with the majority of their land regions in Oklahoma or Texas. Extension nutritionists were contacted via email to obtain information on common fed diets and supplementation formulation (Jason Banta, personal communication; Janna Block, personal communication; Karl Hoppe, personal communication; Jaymelynn Farney, personal communication; Gregory Lardy, personal communication; Ryan Rueter, personal communication; Karla Wilke, personal communication). Those formulations used in the CCSM are fully laid out in Table 3.3. Each diet follows a general pattern: any hay is assumed to be either mid-bloom smooth brome, bermuda, or prairie hay, according to the most common forage species available in the region. In addition to hay was either whole grain corn, corn dry distillers' grains with solubles (CDDGS), a mix of the two, or mid- bloom alfalfa hay. The net energy for each delivered ration and supplementation diet was calculated as weighted average based on the percent of each ingredient and the net energy values of each ingredient (Jurgens et al., 2012; Johnston and Moreau, 2017). While the composition of each diet was crafted to match regional feedstuffs, it is important to note that much like forages, the CCSM

only provides the net energy for the delivered ration and supplement as a whole. The formulation of those diets and overall net energy estimation is determined externally by the user.

Another aspect of this study was to explore the environmental impact of substituting all corn and corn products fed to cow-calf operations with grain sorghum and grain sorghum products. Therefore, after the amount of corn and CDDGS required on dry matter basis was calculated, grain sorghum and grain sorghum distillers' grain (SDDGS) were used to replace corn grain and corn DDGS, respectively, based on net energy maintenance equivalency. Those equivalencies, on a dry matter basis, are as follows: 1.173 kg of grain sorghum was substituted for every 1 kg of whole grain corn and 1.046 kg of SDDGS was substituted for every 1 kg of CDDGS.

To estimate land use, crop yields were obtained for each MLRA. A representative county was chosen for each MLRA and estimates of annual corn, grain sorghum, grass hay, and alfalfa hay yields from 1995 to 2019 were obtained from the National Agriculture Statistics Service (NASS, 2021). Those annual estimates were averaged for each crop for each MLRA. In two cases, no county data was available: grain sorghum yield estimates for counties in North Dakota and alfalfa hay and grass hay yields for counties in Texas. The average sorghum yield of all the counties in South Dakota which are on the North Dakota border were averaged applied to all the MLRAs which laid fully in North Dakota. Texas only reports state-wide average alfalfa yields. Therefore, the average of the state-wide alfalfa and grass hay yields from 1995 to 2019 were used as representative values. The yield values reported by the NASS (2021), were measured in bushels per acre for grain crops or tons per acre for forage crops. These values were adjusted to kilograms per hectare from bushels per acre for grain crops and tons per acre forage crops.

Climate Parameters

Climate plays a very large role in the energy requirement of cattle, as well how much irrigation will be needed to produce feedstuffs. To accommodate these facts, a representative county was chosen from each MLRA and monthly temperature and precipitation data from 1995 to 2019 was gathered for that county from the National Centers for Environmental Information (NOAA, 2021). Where climate information was missing, the average temperature or precipitation of the known records was used.

Land Use

As described before, the CCSM generated the kilograms of dry matter of forage, supplement, and delivered ration required every year to keep each animal at a body condition score of 5 given the parameters provided for genetic potentials and nutritional densities in each MLRA. Those values were averaged for all 24 years in each iteration, then averaged for all 25 iterations to determine the weight of each diet required for each combination of genetics and location in the typical year. The amount of supplement and delivered ration were multiplied by the percent of each feedstuff assumed to be in the given diet. These calculations yielded the dry matter weight of each feedstuff necessary. The kilograms of dry matter of each feedstuff were divided by literature estimates of percent dry matter of each feedstuff which generated the kilograms of feedstuffs on an as-fed basis (Jurgens et al., 2012; Johnston and Moreau, 2017). Because it was assumed that all feedstuffs consumed in each MLRA were grown in that area, the as-fed feedstuff values were divided by the average yield to calculate the hectares required to grow feedstuffs for each feedstuff for each MLRA. In addition, both CDDGS and SDDGS on an as-fed basis were divided by corn and sorghum yield of the appropriate MLRA, respectively.

Interestingly, the amount of land required to grow crops is not necessarily equivalent to the land required to grow feedstuffs for beef production. Because dry distillers' grain is a by-

product of the ethanol process rather than a direct input, its environmental footprint for beef production needs to be scaled (FAO, 2016). One way to perform this scaling, or allocation, is by mass. Dividing the weight of dry distillers' grain with solubles by the weight of the grain before processing produced an allocation percentage (FAO, 2016). This allocation percentage was applied to all resource inputs of dry distillers' grain with solubles, including land, water, and fertilizer. Corn distillers' grain with solubles was allocated 30% of the natural resources used to produce corn, while SDDGS was allocated 32% of the natural resources used to produce sorghum (Johnston, personal communication).

Once the allocations were applied, the total land use for growing feedstuffs was calculated by summing the amount of land necessary to produce each feedstuff required in each diet. If field grain products were used, the amount of land required for feedstuffs was calculated twice (once for corn- based diets and again for sorghum).

Further, the amount of land used for grazing was found by multiplying the number of animals of each class (replacement heifers, bred heifers, and mature cows) in the average year by the stocking rate of that class for each unique scenario. The total amount of land required for beef production was calculated by summing grazing land and crop land. This was also performed twice, where appropriate, to account for use of corn vs sorghum-based products.

Water Use

In beef cattle production, the blue water footprint is the water used for crop irrigation and for cattle to drink (Rotz et al., 2019). Estimating irrigation first requires knowing how much water crops require. This can be done using the Blaney-Criddle methodology (Blaney and Criddle, 1950; Brouwer and Heibloem, 1986). Briefly, the mean monthly temperature for a representative county was used in combination with the mean percentage of daily sunlight hours

for each month based on latitude in order to estimate baseline evapotranspiration for each MLRA. Next, the growing season for each irrigated crop (alfalfa, corn, and sorghum only, as grass hay and grazed forage was assumed to be non-irrigated) was calculated. The Field Crops Usual Planting and Harvesting Dates publication (USDA, 2010) detailed the planting and harvest date for each crop in each state. For corn and sorghum, the beginning of the growing period was set as the beginning date in the most active period of planting for each crop in each state, as appropriate for which state captured the majority of the MLRA of interest. The end of the growing period was the assumed to be the start date plus the number of growing period days specific to each crop outlined in Brouwer and Heibloem (1986). For corn and sorghum, the time between the planting date and the end of the growing period was considered the growing season. For example, the median planting date for corn in North Dakota was May 2 and requires 125 days of growth; therefore, the growing season was May 2 through September 7. For alfalfa, the growing season was considered to begin 40 days before the median first harvest date in each state (Anderson, 2019). The growing season for alfalfa was assumed to end the median day of the last harvest for each state. Data to establish a unique growing period for each crop was available in each state, except for sorghum in North Dakota, which was assumed to be the same as the growing season for sorghum in South Dakota. Once the growing season for each crop was established, development stages were assigned to periods within the growing season for each crop in each state. The length of each development stage for each crop was set according to Brouwer and Heibloem (1986). Next, crop coefficients were introduced to adjust the baseline evapotranspiration for a given crop in a given development stage. These values varied as the crops developed, except for alfalfa. The crop coefficient for alfalfa was assumed to always be 1.05, which is the coefficient recommended for alfalfa for regions with strong winds such as the

Great Plains (Brouwer and Heibloom, 1986). The daily water requirement in a given month for a given crop in a given state was calculated as a weighted average of the number of days the crop was in a given development stage divided by 30 (all months were assumed to have 30 days) multiplied by the appropriate crop coefficient. For example: sorghum in Kansas in June spends 4 days in one development stage and the other 26 days in another development stage; therefore, the equation to determine the daily water requirement for sorghum in Kansas in June is as follows:

$$\left(\frac{4}{30} * 0.35\right) + \left(\frac{26}{30} * 0.75\right) = 0.6967\ mm\ per\ day$$

where 0.35 and 0.75 are crop coefficients for different growing stages in corn. The water requirement for each crop in each state is detailed in Table 3.4. The daily average water requirements were multiplied by 30 to get millimeters of water required per month per crop per state. Once monthly water requirements were found, rainfall from the observed monthly precipitation was retrieved from a representative county in each MLRA (NCEI, NOAA, 2021). The precipitation was converted into millimeters, scaled to the length of the growing season for each crop in each state, and converted into effective rainfall (the amount of rain that sinks deep enough into the soil for crops to use) using the methodology of Brouwer and Heibloem (1986). Irrigation water needs (millimeters) were calculated by subtracting effective rainfall for each crop from the water requirements for each crop in each MLRA. It was assumed that all irrigation had no inefficiencies, such as leaks. The total volume of irrigation water (liters) was found by multiplying the applied water needs for each crop in each MLRA by the land required by the same crop in the same MLRA by 10,000 (square meters in one hectare).

Drinking water for each herd in each unique scenario was estimated using the information in Spencer et al. (2017). A baseline of 31.04 liters water per day was set for a 500 kg dry cow for days where ambient temperature was equal to or less than 4° C. Deviations from that

baseline were a change of 3.785 liters per day per 90.72 kg increase/decrease in body weight, a change of 3.785 liters per day for each 3.9 kg increase/decrease in peak lactation potential, and a change of 3.785 liters per day for every 10° F increase above 4° C in temperature. Using these guidelines, the 31.04 liter per day baseline was adjusted by mean mature cow body weight, average monthly temperature, and peak lactation potential for each unique scenario. The water requirements equation assumed cows to be in peak lactation from May 1 to October 31 and all classes of cattle drank the same amount as the mature cows. These daily estimates were multiplied by 30 to get monthly drinking water per cow, then by multiplied 100 to get monthly drinking water per herd. Next, all months were summed to find an estimate of annual drinking water required per herd. Finally, irrigation water required in the average year was added to annual drinking water per herd to find the blue water footprint for each unique scenario.

Fertilizer Use

Estimates of applied nitrogen, phosphorus, and potassium were determined for each unique scenario. The average annual yield of alfalfa, grass hay, corn grain, and sorghum grain for each MLRA (NASS, USDA, retrieved April 2021) was used in combination with fertilizer recommendations equations for each crop from Gerwing and Gelderman (2005). Grazing land forage was also assumed to be fertilized and was estimated using the equations for grass (Gerwing and Gelderman, 2005), where forage yield for each MLRA was found as described above. The existing soil nutrient variables in the equations were set to zero due to lack of availability of data in each MLRA to account for these variables. Thus, the results for fertilizer estimates are the upper limits of the fertilizer that would likely be applied in practice and are likely slightly overestimated for some production scenarios. Next, the nitrogen fertilizer estimates were converted from pounds per acre to kilogram per hectare. Phosphorus and

potassium estimates were converted from parts per million to kilogram per hectare, assuming the sample depth was 0.15 meters (equivalent to the 6-inch depth as specified by Gerwing and Gelderman (2005)) and assuming bulk density was 1473.7 kilograms per cubed meter (NRCS, 2021). The fertilizer estimates were multiplied by the land allocated for each feedstuff and summed to get total nitrogen, phosphorus, and potassium estimates for each scenario. This process was performed twice: once summing the fertilizer requirements for alfalfa, grass hay, pasture, and corn products, and then again replacing corn products with sorghum products.

Methane

Methane is a by-product of ruminant fermentation and a potent GHG. There are several empirical equations that can be used to estimate methane production. The most common is the IPCC Tier 2 model (IPCC, 2019), which is as follows (modified to account for an annual gross energy intake estimate):

$$EF = \frac{GEI * \left(\frac{Y_m}{100}\right)}{55.65}$$

where EF is the kilograms of methane per head per year, GEI is gross energy intake in megajoules per herd per year, and Ym is the percent of gross energy in feed converted to methane which is set at 7% for animals consuming a ration composed of greater than 75% forage (IPCC, 2019).

The gross energy of each feedstuff was estimated using the chemical composition of each feedstuff (Jurgens et al., 2012) and this equation from Weiss and Tebbe (2019):

$$GE_i = CP_i * 0.056 + F_i * 0.094 + (100 - CP_i - F_i - A_i) * 0.042$$

where GE is gross energy in megajoules per kilogram of the *i*th feedstuff on a dry matter basis, CP is the percent crude protein of the *i*th feedstuff on a dry matter basis, F is percent ether extract of the *i*th feedstuff on a dry matter basis, and A is the ash of the *i*th feedstuff on a dry matter

basis. For each MLRA, the most dominant species from a list of common grasses (big bluestem, grama grass, Kentucky bluegrass, and smooth brome) for which chemical compositions were known was identified. This species was used as a representative value of all the forage produced in that MLRA due to the difficulty of finding complete chemical compositions for other species.

Once the gross energy of each feedstuff was calculated, those values were multiplied by the kilograms of dry matter intake of the supplement, delivered ration, or forage in the average year for each unique scenario modeled. This calculation produced the average annual gross energy intake for each scenario. The IPCC Tier 2 (IPCC, 2019) model was used to estimate the methane produced in each scenario using the gross energy intake specific to each region. The emission factor that resulted detailed the kilograms of methane emitted from each herd in each scenario in the average year. Like land, water, and fertilizer, this process was repeated twice, once using forages and corn products, then again with forages and sorghum products.

Results and Discussion

Each MLRA has a unique combination of mature cow body weight, diet formulation, forage composition and yield, and climate, and the impact of these differences can be seen in Appendix A. These various factors in each MLRA and simulation make it somewhat difficult to evaluate differences between MLRAs. However, some general trends can be found within the results. It should be noted that the values for land, water, and fertilizer reported are the estimates for those resources after the mass allocations for CDDDS and SDDGS have been applied.

Land Use

The estimates for allocated land use are listed in Appendix A (A.2) and are representative of the average year (the average of all 25 iterations of the 24 simulated years). The minimum value for land needed to grow feedstuffs was roughly 31 ha for small, low milking cattle fed

corn-based diets. The maximum amount of land needed to grow feedstuffs was 127 ha used to feed large, high milking cattle with only prairie and alfalfa hay. The average amount of land used to grow feedstuffs was 58 ha if corn products were used and 61 ha if sorghum products were used. In general, diets that did not include grain, or included only dry distillers' grain (see Table 3.3) required more land than diets that included grain. This is because the net energy of diets formulated with grain have a much higher net energy concentration. Therefore, less land is required to meet each animal's net energy needs. However, with all land use discussions, the amount of land required is not the only consideration when discussing sustainability. For example, although diets utilizing only forage-based products require the most land, they also utilize only human-inedible foodstuffs.

When considering the effect of genetic potential on total land used for growing feedstuffs, including both supplementation and the delivered ration, the higher lactation animals required more land than the low lactation animals and the larger animals required more land than the smaller animals, on average, as would be expected. This trend continued regardless of whether corn or sorghum products were used. However, it is interesting to note that lactation was a larger driver of supplemental feed use while grazing pasture than body size. The small, high milking cattle often consumed the most supplemental feed while grazing, followed by the medium, high milking animals. Their smaller size prohibited them from being able to consume enough forage to meet those needs. Thus, those animals were supplemented at a greater rate while grazing pasture than the low lactation animals. However, when grazing land was also included, size became the primary driver of total land use because larger animals required a lower stocking rate and thus more acres of grazable pasture for each 100 head herd. On a per kilogram weaned basis (average weaning weight for each genetic potential), the lower lactation

animals required less land for feedstuffs than high lactation animals with smaller animals being more efficient than larger ones of the same lactation potential (Table 3.5a-b). Conversely, body weight was the primary driver of grazing land efficiency. The small body weight animals used the least amount of grazing land per kilogram weaned, followed by the moderate, high lactation animals. Interestingly, the large, high milking animals used grazing land more efficiently than the moderate and large, low milking cattle, which ranked second to last and last, respectively. Nevertheless, in terms of total land use per kilogram of weaning weight, the smaller animals were the most efficient and higher lactation animals were more efficient than lower lactation animals of the same size. This assumes that enough supplementation can be provided in a cost-effective manner to offset their increased energy and supplementation needs.

The regions that required the least amount of crop land were in the Western areas of Nebraska, Kansas, Oklahoma, and Texas. This is because those regions primarily used by-products for grain feedstuffs, for which only roughly 30% of the total land used for production was allocated to the land use of the herd. In addition, these regions had high grass and alfalfa hay yields and lighter mature animals than those regions further east or north. On the contrary, the regions with the highest demand for land to grow feedstuffs were located in Western North Dakota and Central South Dakota through Central Nebraska. In some cases, the regions with the lowest requirements neighbored the regions with some of the highest requirements. Several factors influenced the differences between regions with high and low crop land requirements. First, the high-demand regions were those that did not feed grain but utilized alfalfa instead. Because alfalfa is less energy-dense, more of it was required to meet the herds' nutritional needs. Second, the high demand regions were, in general, further east or further north than the low demand regions. This is because the high demand regions usually had heavier mature cattle

because the mean body weight of cattle increased further north at the same longitude or further east at the same latitude. Lastly, the high demand regions had lower grass and alfalfa yields than the low demand regions, possibly because of differences in irrigation practices that were not accounted for in this simulation. The regions with the highest demand for grazing land were those located in far West Texas, despite having some of the lightest mature body weights, because forage is often scarce in those areas. Conversely, the regions with the highest stocking rate were in Eastern Kansas and Nebraska where high-quality, intensively managed pastures made up the majority of the grazing land.

The average total amount of land required for diets using corn products was 711 hectares. Conversely, the average total amount of land required for diets using sorghum products was 714 hectares. Grazing was the majority of total land use, accounting for between 70-92% of all hectares required for the herd, irrespective of whether corn or sorghum was used. Because grazing was the primary use for land, small animals were more efficient than large animals in their total land use; and because animals of the same size received the same amount of grazing land and high lactation animals weaned a heavier calf crop, high milking animals were more efficient than low milking animals of the same size. Further, again because grazing land was the majority of land use, regions with very low stocking rates required the most total land.

Water Use

The estimates for allocated irrigation water use are in Appendix A (Table A.3) and all values are representative of the average year as defined in the previous section. The average amount of water used for irrigation is 28,941,643 liters for corn-based diets and 41,129,415 liters for sorghum-based diets. Corn-based rations required less irrigation water than sorghum-based rations in almost every MLRA, contrary to general assumptions about water use of sorghum.

This is due to the fact that while sorghum does have a lower water requirement per plant, it also has a lower yield and a lower net energy concentration. The amount of extra land, and the associated extra water, to produce the same net energy as corn outweighed sorghum's water efficiency. This result may be exacerbated in this study due to the difference in management practices between corn and sorghum production. Corn is often cultivated in a manner to maximize yield while sorghum is often grown in areas where corn cannot be produced, which may bias the calculations in favor of corn simply due to where producers choose to grow sorghum rather than any inherent deficiency in sorghum yield. It is worth noting that in MLRAs where sorghum yields were high, the difference between water allocated to corn products and the water allocated to sorghum products became much narrower than those areas with high corn yield and low sorghum yield. In fact, in MLRA 152B (Southeast Texas) corn yields were lower than sorghum yields (for unknown reasons), and in this region sorghum was a more water-efficient crop. Herds consuming sorghum-based diets required at least 1.5 million fewer liters of allocated water per herd than the same herds fed corn in that region, regardless of the animals' genetic potential. This suggests that if the beef industry switched to sorghum products and crop producers changed management strategies to meet the new demand (and/or sorghum breeders improved yield through breeding), sorghum yields may improve enough to outweigh the advantage of corn-based systems. Though the result of these potential changes is somewhat speculative, it does highlight one potential area whereby the beef industry might decrease its water footprint.

Irrigation demands for different genetic potentials are confounded with climatic and diet differences across regions, making it difficult to determine exactly how much more water efficient one type of animal is compared to another. On average, lactation drove irrigation

demand, similar to land used for growing feedstuffs, because of the extra supplement required over the grazing season. Within lactation potential, heavier animals required more irrigation water than lighter animals, as would be expected. In contrast, when the efficiency of genetic potentials was examined, small, low milking cattle and moderate, low milking cattle required the least amount of irrigation per kilogram of weaning weight. The genetic potential with the third lowest demand for irrigation per kilogram of weaning weight was the small, high milking animals, followed by the large, low milking animals. The moderate, high milking and large, high milking cattle were the least efficient users of irrigation water.

Drinking water, like irrigation water, is entangled with differences in body size and climate between regions. Nonetheless, body weight was the driving factor in drinking water consumption with large animals requiring more water than smaller ones. Because of the added demands of milk production, high lactating animals required more drinking water than low lactation animals of the same size. Conversely, lactation seemed to have a greater impact on drinking water efficiency than body weight. Small and moderate weight cattle with high lactation potential used the least drinking water per kilogram of calf weaned. However, small, low milking animals were slightly more efficient with their drinking water than large, high milking cattle which were slightly more efficient than moderate, low milking cattle. The least water efficient animals were large, low lactation animals requiring much more drinking water per kilogram of weaning weight, relative to other genetic potentials. Drinking water comprised anywhere from 1-23.5% of blue water use (8.76% average) when corn products were used in the diet. When sorghum products were used, drinking water only accounted for 1-11% of the blue water footprint (4.8% average). The difference between the percentages is due to the increased need for land, and subsequently irrigation, of sorghum-based diets while water intake is held constant.

The variation in percent drinking water reported in this study resulted from decreased irrigation requirements due to diet formulation or precipitation in some regions while simultaneously having increased drinking water requirements due to either heavier than average mature cattle or increased temperature. Rotz et al. (2019) reported that 5% or more of the beef's industry blue water footprint was from drinking water, which is somewhat lower than the estimates reported here. The reason for the discrepancy is Rotz et al. (2019) included regions in the West and Southwest United States which require drastically more irrigation than the regions examined here.

Regional variation was clearly evident in water requirement estimation. To begin with, dissimilarities in diet formulation and body weight lead to large gaps in irrigation requirements. The minimum value for irrigation was 4,859,473 liters, which was for small, low milking cattle a diet comprised of prairie hay and CDDGS. The maximum amount of water used to grow feedstuffs was 157,706,847 liters to feed prairie hay and alfalfa to large, high milking animals. The differences between the regions with the highest (Western South Dakota) and lowest (Western Texas) irrigation demands are multifaceted. Firstly, the size and lactation potential of the animals vary greatly (see Appendix A for requirement differences due to genetic potentials). The animals in Western South Dakota weighed, on average 647 kilograms, compared to the animals in Western Texas, which weighed 459.5 kilograms. Assuming each animal ate 2.7% of its body weight per day, the heavier animals ate 5.0625 kilograms more dry matter per day. As a herd, they ate 506 kilograms more per day. In addition, the animals with the most irrigation demands were in the North West diet region. As shown in Table 3, the animals in the North West diet region are fed alfalfa instead of grain. Alfalfa is less energy dense than grain meaning more of it is required to obtain the same net energy. This fact, in addition to alfalfa being a water

intensive crop and MLRA 63A receiving relatively little precipitation compared to regions further east, meant that substantial amounts of water must be supplied via irrigation. Conversely, the region with the lowest irrigation demand was in the South West. While 77E is an arid climate, the animals are fed dry distillers' grain and prairie hay. Prairie hay was assumed to be non-irrigated, and most of the water footprint from dry distillers' grain is allocated to production of the crop itself rather than to DDGS. While the differences between the irrigation extremes is large, they are understandable in the context of the assumptions made in this study. Similarly, the regional differences in drinking water were logical when put in context. The regions with the greatest demand for drinking water were in far Southern Texas where the high average temperature required the animals to drink more. The Western regions of the Great Plains demanded less drinking water because the animals there are smaller, on average, than those in the Eastern regions.

The average blue water use (irrigation and drinking water) across all regions was 30,588,949 liters and 42,776,720 liters in the average year for diets using corn and sorghum-based products, respectively. The primary driver between the difference in blue water use estimates was the difference in land, and associated irrigation, required by each crop to grow the requisite net energy. Consequently, the regions with the largest blue water use were those in the Northwest Dakotas while the regions with the lowest blue water use were in West Texas. Again, while these results seem unexpected, they are understandable given the assumptions of the model; namely, diet formulations in different regions and the assumption grass hay and grazing land were not irrigated. In general, high lactation animals required more blue water than low lactation animals, with larger animals using more blue water than smaller animals of the same lactation potential, as would be expected. This trend held for both corn and sorghum diets. While

grazing land was assumed to not be irrigated, harvested feedstuffs were irrigated in MLRAs where precipitation did not meet the water needs of the crop. Therefore, the increased need for supplementation of high lactation animals resulted in an increased need for harvested feedstuffs and an increased blue water use compared to low lactation animals of the same weight. Curiously, the genetic potentials followed an unusual pattern when blue water use was scaled by weaning weight. The most efficient animals were the small and moderate low lactation animals because of their limited irrigation water use. Next were the small, high milking cattle followed by the large, low milking cattle. While the large, low lactation animals used less blue water, the slightly larger calf of the small, high milking animal showed the latter genetic potential to be more efficient in its average blue water use. Finally, as with irrigation water, the moderate and large high lactation animals used the most blue water per kilogram of calf weaned.

Fertilizer Use

Fertilizer amounts for each scenario are detailed in Appendix A (Table A.4). It is important to remember that the values reported here are the maximum amount of nutrients that would be recommended to be applied based on feedstuff yield because no data was available on starting soil fertility differences in the MLRA regions. These values did not take any existing soil nutrients, recycling done by the animals, or left-over plant residue into account. Thus, these values are a gross generalization and likely overestimate the amount of fertilizer required (in some cases by a wide margin) and a more sophisticated method with soil fertility data specific to each region would be required to make specific policy or management decisions.

The difference in fertilizer between corn-based diets and sorghum-based diets is negligible. The average nitrogen for corn diets was 26,532 kilograms per year and 26,524 kilograms per year for sorghum diets. In addition, the average phosphorus was 630,014

kilograms per year for corn diets and 630,021 kilograms per year for sorghum diets. Lastly, the potassium estimates were 1,803,550 kilograms per year and 1,803,400 kilograms per year for corn and sorghum diets, respectively. If the beef industry were to entirely switch over to sorghum and practices stayed as they currently stand, there would be little difference in the amount of fertilizer applied for feedstuffs. However, if the beef industry switched to sorghum and practices changed to meet new demand, it is unclear how fertilizer application would change. Sorghum yields would likely increase, requiring fewer hectares, but fertilizer application per hectare may also increase to produce those higher yields.

Mature body weight was the characteristic that largely determined relative nitrogen use between genetic potentials, regardless of diet formulation. Because larger cattle required more land for grazing, they also required more nitrogen than smaller cattle. Within each weight category, high milking animals had more nitrogen use than low lactation animals due to the increased supplement and delivered rations provided to the high milking cattle. This pattern held for nitrogen use scaled by weaning weight, with small, high lactating animals being the most efficient and large, low lactating animals being the least efficient. This trend did not continue in phosphorus or potassium estimates for each genetic potential. Instead, those nutrients did not follow a simple pattern. Instead, the large, high lactation animals were followed by the medium, high milking cattle, then the large, low lactation animals. The small, high milking animals were next, while the medium, low milking and small, low milking cattle required the least phosphorous and potassium fertilizer. Here, the trend may have been partially driven by lactation potential and the additional supplement high milking animals tended to require; however, the greater area of grazing land used by the large, low lactation cattle outweighed the small, high lactation animals in terms of fertilizer requirements.

Regionally, the highest nitrogen use was in Central Texas where the vast areas of land allocated to each animal increased the gross amount of nitrogen applied to grazing land. In addition, the heavier body weights in these regions (compared to West Texas and Oklahoma which had even more diluted stocking rates), increased the requirement for grain-based feedstuffs, which, in turn, further increased nitrogen application. The regions with the least nitrogen application were those in Western North and South Dakota where alfalfa, which requires no applied nitrogen, replaced grain. Interestingly, those regions also required the most phosphorus and potassium, precisely because alfalfa typically requires those nutrients to be applied in large quantities. Alternatively, the regions with the least amount of phosphorus and potassium applied were in East Texas, where the only grain product being fed was CDDGS/SDDGS and there was less demand for feedstuffs due to lighter weight cattle and denser stocking rate, which reduced the need for those nutrients.

Methane Production

The values of estimated methane emissions for each scenario are in Appendix A (Table A.5). The average methane for all scenarios when corn products were used was 8,898 kilograms per herd per year. The average methane for all scenarios when sorghum products were used was 8,925 kilograms per herd per year. Methane production tends to increase as forage intake increases (IPCC, 2019), therefore, diets formulated with grains were compared to diets not including grains. For diets that used corn products, the average yearly methane production for the herd was 8,866 kilograms. For diets that used sorghum products, the average yearly methane production was 8,899 kilograms for the herd. When animals were only fed harvested or grazed forages, an average of 9,059 kilograms of methane per herd per year was produced. While these differences are not exceedingly large, this is because the majority of the diets fed were comprised

of forage, regardless of whether they included grain-based components or not. In addition, harvested forages have a lower net energy concentration than grains, which means more harvested forages are required to meet the same energy requirements. Further, no diets were formulated in such a way to take advantage of the more favorable methane conversion rate seen when animals are fed a diet of greater than 25% forage (IPCC, 2019).

The increase in kilograms of methane from diets comprised of only harvested forages was inextricably confounded with larger mature body weight. Larger animals produced more methane per year than smaller animals, and the high lactation animals produced more methane than the low lactation animals of the same size. This trend held for both corn and sorghum product diets. The IPCC Tier 2 model (IPCC, 2019) assumed that 7% of all gross energy intake was converted into methane. Therefore, the genetic potentials that consumed the most also produced the most methane. The range in methane efficiency was between the different genetic potentials was 285 and 31 grams of methane per kilogram of weaning weight (very similar estimates for sorghum). For comparison, Rotz et al, (2019) reported 370 grams per kilogram of carcass weight for the national cow-calf sector; however, this value also includes methane from manure and is scaled by carcass weight of harvested beef, rather than the carcass weight of the cow-calf sector. Comparisons of the genetic potentials showed the small, high lactation cattle produced the least amount of methane per kilogram of weaning weight, closely followed by small, low lactation animals. Curiously, the next most efficient genetic potentials were moderate and large, high milking cattle. Finally, the moderate and large low lactation cattle were the had the greatest methane yields.

No clear pattern emerged when the methane production of different regions was compared. The regions with the greatest methane production clustered around Central Texas and

Western North Dakota. For a combination of reasons (cattle size, forage energy, and diet formulation), the animals in these regions tended to require more gross energy. Conversely, regions with the least methane production were centered around Eastern Kansas and Nebraska, as well as West Texas. Likely the same combination of reasons caused the animals in these regions to require less gross energy, but there were no clear patterns that emerged to explain these differences.

Conclusions

Using current practices, feeding corn and corn products rather than grain sorghum and grain sorghum products would lead to a lower land and water footprint for the beef industry. However, in regions where sorghum yields are equivalent or higher than corn, sorghum-based diets have a distinct advantage in irrigation requirements. Because of this, the advantage noted for corn-based diets could change if sorghum was grown on higher-quality land that is generally allocated to corn production, or if sorghum genetic improvements substantially improved yield in the future. Still, the difference between the two crops is slim for the cow-calf sector due to the relatively low levels of grain fed. It is unclear how much wider the margin would be when applied to the feedlot sector, where higher-concentrate diets are commonly fed.

Differences between genetic potential for milk and mature weight demonstrated that large, high lactation animals require more resources and emit more methane than other combinations. High lactation animals had a larger environmental footprint than low lactation animals of equivalent size because of their increased energy requirements. Efficiencies of natural resource use per kilogram of calf weaned suggest small, high lactation animals often have the smallest environmental impact per unit of product. However, it is worth noting weaning weight estimates were based on national averages and certain assumptions. Actual weaning weights for each

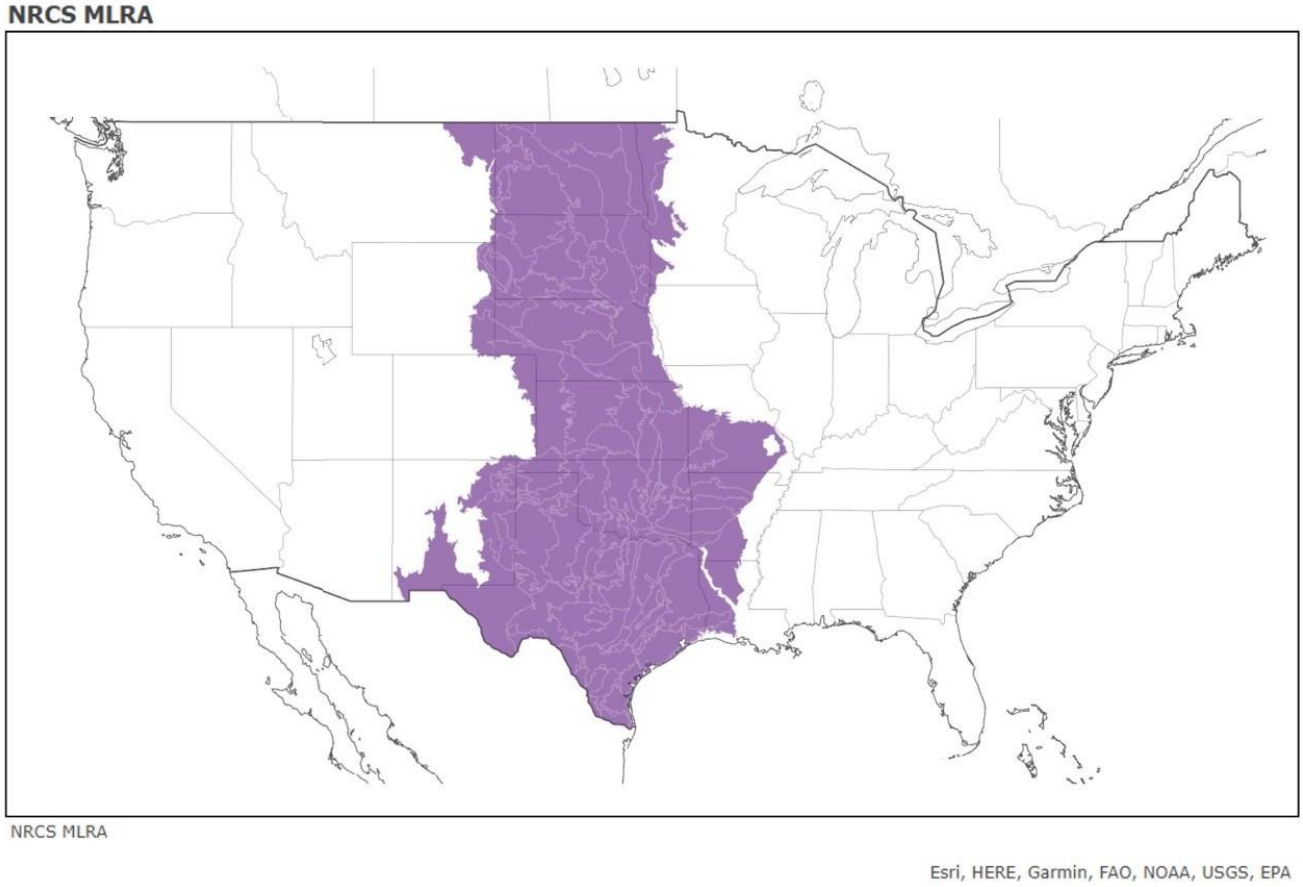
genetic potential will likely vary by region. For example, larger body weight animals may have larger calves under conditions where forage production is greater per hectare than the same size animals under different conditions. Therefore, optimal genetic potential may change within region.

Further, the model presented here assumes land was an unlimited resource, or as much land as was necessary to meet each herd's needs was available. The optimal genetic potential, choice of grain, and overall environmental impact may change if those factors were to be evaluated on a limited land basis.

Each MLRA is a unique region in the Great Plains with its own combination of climate, diet, stocking rate, and genetic potentials. All suggestions of changing production practices to better meet sustainability goals need to be considered on a regional, if not operational level for feasibility and effectiveness. Lastly, all environmentally sustainable practices need to be balanced with social and economic factors.

Figure 3.1

Major Land Resource Areas of the Great Plains



Adapted from ArcGIS Online, 2021

Table 3.1

Mature cow bodyweight, lactation potential, stocking rate, and annual forage production for various regions across the Great Plains

MLRA	Mature Cow Bodyweight (kg)	Peak Lactation (kg milk/day)	Hectares per Cow-calf Pair	Hectares per Bred Heifer	Hectares per Replacement Heifer	Forage Production (kg/ha)
102A-LH	677.0	11	3.20	2.70	1.85	1628.05
102A-LL	677.0	8	3.20	2.70	1.85	1628.05
102A-MH	608.0	11	2.90	2.43	1.66	1628.05
102A-ML	608.0	8	2.90	2.43	1.66	1628.05
102A-SH	539.0	11	2.50	2.16	1.47	1628.05
102A-SL	539.0	8	2.50	2.16	1.47	1628.05
102B-LH	677.0	11	3.20	2.70	1.85	1764.17
102B-LL	677.0	8	3.20	2.70	1.85	1764.17
102B-MH	608.0	11	2.90	2.43	1.66	1764.17
102B-ML	608.0	8	2.90	2.43	1.66	1764.17
102B-SH	539.0	11	2.50	2.16	1.47	1764.17
102B-SL	539.0	8	2.50	2.16	1.47	1764.17
102C-LH	677.0	11	3.20	2.70	1.85	1535.45
102C-LL	677.0	8	3.20	2.70	1.85	1535.45
102C-MH	608.0	11	2.90	2.43	1.66	1535.45
102C-ML	608.0	8	2.90	2.43	1.66	1535.45
102C-SH	539.0	11	2.50	2.16	1.47	1535.45
102C-SL	539.0	8	2.50	2.16	1.47	1535.45
106-LH	582.5	11	2.60	2.24	1.53	1808.88
106-LL	582.5	8	2.60	2.24	1.53	1808.88
106-MH	537.0	11	2.40	2.07	1.41	1808.88
106-ML	537.0	8	2.40	2.07	1.41	1808.88
106-SH	491.5	11	2.20	1.89	1.29	1808.88
106-SL	491.5	8	2.20	1.89	1.29	1808.88

112-LH	582.5	11	2.60	2.24	1.53	1907.92
112-LL	582.5	8	2.60	2.24	1.53	1907.92
112-MH	537.0	11	2.40	2.07	1.41	1907.92
112-ML	537.0	8	2.40	2.07	1.41	1907.92
112-SH	491.5	11	2.20	1.89	1.29	1907.92
112-SL	491.5	8	2.20	1.89	1.29	1907.92
116A-LH	582.5	11	2.60	2.24	1.53	1907.61
116A-LL	582.5	8	2.60	2.24	1.53	1907.61
116A-MH	537.0	11	2.40	2.07	1.41	1907.61
116A-ML	537.0	8	2.40	2.07	1.41	1907.61
116A-SH	491.5	11	2.20	1.89	1.29	1907.61
116A-SL	491.5	8	2.20	1.89	1.29	1907.61
116B-LH	582.5	11	2.60	2.24	1.53	1907.49
116B-LL	582.5	8	2.60	2.24	1.53	1907.49
116B-MH	537.0	11	2.40	2.07	1.41	1907.49
116B-ML	537.0	8	2.40	2.07	1.41	1907.49
116B-SH	491.5	11	2.20	1.89	1.29	1907.49
116B-SL	491.5	8	2.20	1.89	1.29	1907.49
117-LH	582.5	11	2.60	2.24	1.53	1907.78
117-LL	582.5	8	2.60	2.24	1.53	1907.78
117-MH	537.0	11	2.40	2.07	1.41	1907.78
117-ML	537.0	8	2.40	2.07	1.41	1907.78
117-SH	491.5	11	2.20	1.89	1.29	1907.78
117-SL	491.5	8	2.20	1.89	1.29	1907.78
118A-LH	582.5	11	2.60	2.24	1.53	1907.72
118A-LL	582.5	8	2.60	2.24	1.53	1907.72
118A-MH	537.0	11	2.40	2.07	1.41	1907.72
118A-ML	537.0	8	2.40	2.07	1.41	1907.72
118A-SH	491.5	11	2.20	1.89	1.29	1907.72

118A-SL	491.5	8	2.20	1.89	1.29	1907.72
118B-LH	582.5	11	2.60	2.24	1.53	2036.45
118B-LL	582.5	8	2.60	2.24	1.53	2036.45
118B-MH	537.0	11	2.40	2.07	1.41	2036.45
118B-ML	537.0	8	2.40	2.07	1.41	2036.45
118B-SH	491.5	11	2.20	1.89	1.29	2036.45
118B-SL	491.5	8	2.20	1.89	1.29	2036.45
119-LH	582.5	11	2.60	2.24	1.53	2040.57
119-LL	582.5	8	2.60	2.24	1.53	2040.57
119-MH	537.0	11	2.40	2.07	1.41	2040.57
119-ML	537.0	8	2.40	2.07	1.41	2040.57
119-SH	491.5	11	2.20	1.89	1.29	2040.57
119-SL	491.5	8	2.20	1.89	1.29	2040.57
133B-LH	582.5	11	2.60	2.24	1.53	1496.87
133B-LL	582.5	8	2.60	2.24	1.53	1496.87
133B-MH	537.0	11	2.40	2.07	1.41	1496.87
133B-ML	537.0	8	2.40	2.07	1.41	1496.87
133B-SH	491.5	11	2.20	1.89	1.29	1496.87
133B-SL	491.5	8	2.20	1.89	1.29	1496.87
135B-LH	582.5	11	2.60	2.24	1.53	1883.15
135B-LL	582.5	8	2.60	2.24	1.53	1883.15
135B-MH	537.0	11	2.40	2.07	1.41	1883.15
135B-ML	537.0	8	2.40	2.07	1.41	1883.15
135B-SH	491.5	11	2.20	1.89	1.29	1883.15
135B-SL	491.5	8	2.20	1.89	1.29	1883.15
150A-LH	582.5	11	2.60	2.24	1.53	3149.43
150A-LL	582.5	8	2.60	2.24	1.53	3149.43
150A-MH	537.0	11	2.40	2.07	1.41	3149.43
150A-ML	537.0	8	2.40	2.07	1.41	3149.43

150A-SH	491.5	11	2.20	1.89	1.29	3149.43
150A-SL	491.5	8	2.20	1.89	1.29	3149.43
150B-LH	582.5	11	2.60	2.24	1.53	2411.66
150B-LL	582.5	8	2.60	2.24	1.53	2411.66
150B-MH	537.0	11	2.40	2.07	1.41	2411.66
150B-ML	537.0	8	2.40	2.07	1.41	2411.66
150B-SH	491.5	11	2.20	1.89	1.29	2411.66
150B-SL	491.5	8	2.20	1.89	1.29	2411.66
152B-LH	582.5	11	2.60	2.24	1.53	1756.50
152B-LL	582.5	8	2.60	2.24	1.53	1756.50
152B-MH	537.0	11	2.40	2.07	1.41	1756.50
152B-ML	537.0	8	2.40	2.07	1.41	1756.50
152B-SH	491.5	11	2.20	1.89	1.29	1756.50
152B-SL	491.5	8	2.20	1.89	1.29	1756.50
42-LH	550.5	11	17.0	14.51	9.9	536.65
42-LL	550.5	8	17.0	14.51	9.9	536.65
42-MH	505.0	11	16.0	13.31	9.08	536.65
42-ML	505.0	8	16.0	13.31	9.08	536.65
42-SH	459.5	11	14.0	12.11	8.26	536.65
42-SL	459.5	8	14.0	12.11	8.26	536.65
53A-LH	635.0	11	7.5	6.34	4.33	1192.45
53A-LL	635.0	8	7.50	6.34	4.33	1192.45
53A-MH	582.0	11	6.80	5.82	3.97	1192.45
53A-ML	582.0	8	6.80	5.82	3.97	1192.45
53A-SH	529.0	11	6.20	5.29	3.61	1192.45
53A-SL	529.0	8	6.20	5.29	3.61	1192.45
53B-LH	647.0	11	3.60	3.03	2.07	1048.00
53B-LL	647.0	8	3.60	3.03	2.07	1048.00
53B-MH	600.0	11	3.30	2.81	1.91	1048.00

53B-ML	600.0	8	3.30	2.81	1.91	1048.00
53B-SH	553.0	11	3.00	2.59	1.76	1048.00
53B-SL	553.0	8	3.00	2.59	1.76	1048.00
53C-LH	647.0	11	3.60	3.03	2.07	1269.92
53C-LL	647.0	8	3.60	3.03	2.07	1269.92
53C-MH	600.0	11	3.30	2.81	1.91	1269.92
53C-ML	600.0	8	3.30	2.81	1.91	1269.92
53C-SH	553.0	11	3.00	2.59	1.76	1269.92
53C-SL	553.0	8	3.00	2.59	1.76	1269.92
54-LH	635.0	11	7.50	6.34	4.33	854.76
54-LL	635.0	8	7.50	6.34	4.33	854.76
54-MH	582.0	11	6.80	5.82	3.97	854.76
54-ML	582.0	8	6.80	5.82	3.97	854.76
54-SH	529.0	11	6.20	5.29	3.61	854.76
54-SL	529.0	8	6.20	5.29	3.61	854.76
55A-LH	647.0	11	3.60	3.03	2.07	1504.19
55A-LL	647.0	8	3.60	3.03	2.07	1504.19
55A-MH	600.0	11	3.30	2.81	1.91	1504.19
55A-ML	600.0	8	3.30	2.81	1.91	1504.19
55A-SH	553.0	11	3.00	2.59	1.76	1504.19
55A-SL	553.0	8	3.00	2.59	1.76	1504.19
55B-LH	677.0	11	3.20	2.70	1.85	1336.89
55B-LL	677.0	8	3.20	2.70	1.85	1336.89
55B-MH	608.0	11	2.90	2.43	1.66	1336.89
55B-ML	608.0	8	2.90	2.43	1.66	1336.89
55B-SH	539.0	11	2.50	2.16	1.47	1336.89
55B-SL	539.0	8	2.50	2.16	1.47	1336.89
55C-LH	647.0	11	3.60	3.03	2.07	1456.93
55C-LL	647.0	8	3.60	3.03	2.07	1456.93

55C-MH	600.0	11	3.30	2.81	1.91	1456.93
55C-ML	600.0	8	3.30	2.81	1.91	1456.93
55C-SH	553.0	11	3.00	2.59	1.76	1456.93
55C-SL	553.0	8	3.00	2.59	1.76	1456.93
56-LH	677.0	11	3.20	2.7	1.85	1788.63
56-LL	677.0	8	3.20	2.7	1.85	1788.63
56-MH	608.0	11	2.90	2.43	1.66	1788.63
56-ML	608.0	8	2.90	2.43	1.66	1788.63
56-SH	539.0	11	2.50	2.16	1.47	1788.63
56-SL	539.0	8	2.50	2.16	1.47	1788.63
58C-LH	635.0	11	7.50	6.34	4.33	556.33
58C-LL	635.0	8	7.50	6.34	4.33	556.33
58C-MH	582.0	11	6.80	5.82	3.97	556.33
58C-ML	582.0	8	6.80	5.82	3.97	556.33
58C-SH	529.0	11	6.20	5.29	3.61	556.33
58C-SL	529.0	8	6.20	5.29	3.61	556.33
58D-LH	635.0	11	7.50	6.34	4.33	719.07
58D-LL	635.0	8	7.50	6.34	4.33	719.07
58D-MH	582.0	11	6.80	5.82	3.97	719.07
58D-ML	582.0	8	6.80	5.82	3.97	719.07
58D-SH	529.0	11	6.20	5.29	3.61	719.07
58D-SL	529.0	8	6.20	5.29	3.61	719.07
60A-LH	635.0	11	7.50	6.34	4.33	723.74
60A-LL	635.0	8	7.50	6.34	4.33	723.74
60A-MH	582.0	11	6.80	5.82	3.97	723.74
60A-ML	582.0	8	6.80	5.82	3.97	723.74
60A-SH	529.0	11	6.20	5.29	3.61	723.74
60A-SL	529.0	8	6.20	5.29	3.61	723.74
61-LH	635.0	11	7.50	6.34	4.33	983.57

61-LL	635.0	8	7.50	6.34	4.33	983.57
61-MH	582.0	11	6.80	5.82	3.97	983.57
61-ML	582.0	8	6.80	5.82	3.97	983.57
61-SH	529.0	11	6.20	5.29	3.61	983.57
61-SL	529.0	8	6.20	5.29	3.61	983.57
62-LH	635.0	11	7.50	6.34	4.33	917.48
62-LL	635.0	8	7.50	6.34	4.33	917.48
62-MH	582.0	11	6.80	5.82	3.97	917.48
62-ML	582.0	8	6.80	5.82	3.97	917.48
62-SH	529.0	11	6.20	5.29	3.61	917.48
62-SL	529.0	8	6.20	5.29	3.61	917.48
63A-LH	647.0	11	3.60	3.03	2.07	964.47
63A-LL	647.0	8	3.60	3.03	2.07	964.47
63A-MH	600.0	11	3.30	2.81	1.91	964.47
63A-ML	600.0	8	3.30	2.81	1.91	964.47
63A-SH	553.0	11	3.00	2.59	1.76	964.47
63A-SL	553.0	8	3.00	2.59	1.76	964.47
63B-LH	647.0	11	3.60	3.03	2.07	1092.44
63B-LL	647.0	8	3.60	3.03	2.07	1092.44
63B-MH	600.0	11	3.30	2.81	1.91	1092.44
63B-ML	600.0	8	3.30	2.81	1.91	1092.44
63B-SH	553.0	11	3.00	2.59	1.76	1092.44
63B-SL	553.0	8	3.00	2.59	1.76	1092.44
64-LH	635.0	11	7.50	6.34	4.33	851.92
64-LL	635.0	8	7.50	6.34	4.33	851.92
64-MH	582.0	11	6.80	5.82	3.97	851.92
64-ML	582.0	8	6.80	5.82	3.97	851.92
64-SH	529.0	11	6.20	5.29	3.61	851.92
64-SL	529.0	8	6.20	5.29	3.61	851.92

65-LH	647.0	11	3.60	3.03	2.07	1133.99
65-LL	647.0	8	3.60	3.03	2.07	1133.99
65-MH	600.0	11	3.30	2.81	1.91	1133.99
65-ML	600.0	8	3.30	2.81	1.91	1133.99
65-SH	553.0	11	3.00	2.59	1.76	1133.99
65-SL	553.0	8	3.00	2.59	1.76	1133.99
66-LH	647.0	11	3.60	3.03	2.07	1122.77
66-LL	647.0	8	3.60	3.03	2.07	1122.77
66-MH	600.0	11	3.30	2.81	1.91	1122.77
66-ML	600.0	8	3.30	2.81	1.91	1122.77
66-SH	553.0	11	3.00	2.59	1.76	1122.77
66-SL	553.0	8	3.00	2.59	1.76	1122.77
67A-LH	635.0	11	7.50	6.34	4.33	577.63
67A-LL	635.0	8	7.50	6.34	4.33	577.63
67A-MH	582.0	11	6.80	5.82	3.97	577.63
67A-ML	582.0	8	6.80	5.82	3.97	577.63
67A-SH	529.0	11	6.20	5.29	3.61	577.63
67A-SL	529.0	8	6.20	5.29	3.61	577.63
70A-LH	550.5	11	17.0	14.51	9.9	505.44
70A-LL	550.5	8	17.0	14.51	9.9	505.44
70A-MH	505.0	11	16.0	13.31	9.08	505.44
70A-ML	505.0	8	16.0	13.31	9.08	505.44
70A-SH	459.5	11	14.0	12.11	8.26	505.44
70A-SL	459.5	8	14.0	12.11	8.26	505.44
70B-LH	550.5	11	17.0	14.51	9.9	579.85
70B-LL	550.5	8	17.0	14.51	9.9	579.85
70B-MH	505.0	11	16.0	13.31	9.08	579.85
70B-ML	505.0	8	16.0	13.31	9.08	579.85
70B-SH	459.5	11	14.0	12.11	8.26	579.85

70B-SL	459.5	8	14.0	12.11	8.26	579.85
71-LH	647.0	11	3.60	3.03	2.07	1369.40
71-LL	647.0	8	3.60	3.03	2.07	1369.40
71-MH	600.0	11	3.30	2.81	1.91	1369.40
71-ML	600.0	8	3.30	2.81	1.91	1369.40
71-SH	553.0	11	3.00	2.59	1.76	1369.40
71-SL	553.0	8	3.00	2.59	1.76	1369.40
72-LH	550.5	11	17.0	14.51	9.9	805.36
72-LL	550.5	8	17.0	14.51	9.9	805.36
72-MH	505.0	11	16.0	13.31	9.08	805.36
72-ML	505.0	8	16.0	13.31	9.08	805.36
72-SH	459.5	11	14.0	12.11	8.26	805.36
72-SL	459.5	8	14.0	12.11	8.26	805.36
73-LH	580.5	11	6.80	5.80	3.96	1279.56
73-LL	580.5	8	6.80	5.80	3.96	1279.56
73-MH	535.0	11	6.30	5.32	3.63	1279.56
73-ML	535.0	8	6.30	5.32	3.63	1279.56
73-SH	489.5	11	5.80	4.90	3.34	1279.56
73-SL	489.5	8	5.80	4.90	3.34	1279.56
74-LH	580.5	11	6.80	5.80	3.96	1852.12
74-LL	580.5	8	6.80	5.80	3.96	1852.12
74-MH	535.0	11	6.30	5.32	3.63	1852.12
74-ML	535.0	8	6.30	5.32	3.63	1852.12
74-SH	489.5	11	5.80	4.90	3.34	1852.12
74-SL	489.5	8	5.80	4.90	3.34	1852.12
75-LH	647.0	11	3.60	3.03	2.07	1609.32
75-LL	647.0	8	3.60	3.03	2.07	1609.32
75-MH	600.0	11	3.30	2.81	1.91	1609.32
75-ML	600.0	8	3.30	2.81	1.91	1609.32

75-SH	553.0	11	3.00	2.59	1.76	1609.32
75-SL	553.0	8	3.00	2.59	1.76	1609.32
76-LH	582.5	11	2.60	2.24	1.53	1912.63
76-LL	582.5	8	2.60	2.24	1.53	1912.63
76-MH	537.0	11	2.40	2.07	1.41	1912.63
76-ML	537.0	8	2.40	2.07	1.41	1912.63
76-SH	491.5	11	2.20	1.89	1.29	1912.63
76-SL	491.5	8	2.20	1.89	1.29	1912.63
77A-LH	550.5	11	17.0	14.51	9.9	727.09
77A-LL	550.5	8	17.0	14.51	9.9	727.09
77A-MH	505.0	11	16.0	13.31	9.08	727.09
77A-ML	505.0	8	16.0	13.31	9.08	727.09
77A-SH	459.5	11	14.0	12.11	8.26	727.09
77A-SL	459.5	8	14.0	12.11	8.26	727.09
77B-LH	550.5	11	17.0	14.51	9.9	1020.87
77B-LL	550.5	8	17.0	14.51	9.9	1020.87
77B-MH	505.0	11	16.0	13.31	9.08	1020.87
77B-ML	505.0	8	16.0.	13.31	9.08	1020.87
77B-SH	459.5	11	14.0	12.11	8.26	1020.87
77B-SL	459.5	8	14.0	12.11	8.26	1020.87
77C-LH	550.5	11	17.0	14.51	9.9	764.07
77C-LL	550.5	8	17.0	14.51	9.9	764.07
77C-MH	505.0	11	16.0	13.31	9.08	764.07
77C-ML	505.0	8	16.0	13.31	9.08	764.07
77C-SH	459.5	11	14.0	12.11	8.26	764.07
77C-SL	459.5	8	14.0	12.11	8.26	764.07
77D-LH	550.5	11	17.0	14.51	9.9	584.85
77D-LL	550.5	8	17.0	14.51	9.9	584.85
77D-MH	505.0	11	16.0	13.31	9.08	584.85

77D-ML	505.0	8	16.0	13.31	9.08	584.85
77D-SH	459.5	11	14.0	12.11	8.26	584.85
77D-SL	459.5	8	14.0	12.11	8.26	584.85
77E-LH	550.5	11	17.0	14.51	9.9	940.71
77E-LL	550.5	8	17.0	14.51	9.9	940.71
77E-MH	505.0	11	16.0	13.31	9.08	940.71
77E-ML	505.0	8	16.0	13.31	9.08	940.71
77E-SH	459.5	11	14.0	12.11	8.26	940.71
77E-SL	459.5	8	14.0	12.11	8.26	940.71
78A-LH	550.5	11	17.0	14.51	9.9	1438.80
78A-LL	550.5	8	17.0	14.51	9.9	1438.80
78A-MH	505.0	11	16.0	13.31	9.08	1438.80
78A-ML	505.0	8	16.0	13.31	9.08	1438.80
78A-SH	459.5	11	14.0	12.11	8.26	1438.80
78A-SL	459.5	8	14.0	12.11	8.26	1438.80
78B-LH	550.5	11	17.0	14.51	9.9	951.95
78B-LL	550.5	8	17.0	14.51	9.9	951.95
78B-MH	505.0	11	16.0	13.31	9.08	951.95
78B-ML	505.0	8	16.0	13.31	9.08	951.95
78B-SH	459.5	11	14.0	12.11	8.26	951.95
78B-SL	459.5	8	14.0	12.11	8.26	951.95
78C-LH	550.5	11	17.0	14.51	9.9	1300.81
78C-LL	550.5	8	17.0	14.51	9.9	1300.81
78C-MH	505.0	11	16.0	13.31	9.08	1300.81
78C-ML	505.0	8	16.0	13.31	9.08	1300.81
78C-SH	459.5	11	14.0	12.11	8.26	1300.81
78C-SL	459.5	8	14.0	12.11	8.26	1300.81
79-LH	580.5	11	6.80	5.80	3.96	1632.32
79-LL	580.5	8	6.80	5.80	3.96	1632.32

79-MH	535.0	11	6.30	5.32	3.63	1632.32
79-ML	535.0	8	6.30	5.32	3.63	1632.32
79-SH	489.5	11	5.80	4.90	3.34	1632.32
79-SL	489.5	8	5.80	4.90	3.34	1632.32
80A-LH	580.5	11	6.80	5.80	3.96	1991.36
80A-LL	580.5	8	6.80	5.80	3.96	1991.36
80A-MH	535.0	11	6.30	5.32	3.63	1991.36
80A-ML	535.0	8	6.30	5.32	3.63	1991.36
80A-SH	489.5	11	5.80	4.90	3.34	1991.36
80A-SL	489.5	8	5.80	4.90	3.34	1991.36
80B-LH	580.5	11	6.80	5.80	3.96	1576.79
80B-LL	580.5	8	6.80	5.80	3.96	1576.79
80B-MH	535.0	11	6.30	5.32	3.63	1576.79
80B-ML	535.0	8	6.30	5.32	3.63	1576.79
80B-SH	489.5	11	5.80	4.90	3.34	1576.79
80B-SL	489.5	8	5.80	4.90	3.34	1576.79
81A-LH	550.5	11	17.0	14.51	9.9	798.61
81A-LL	550.5	8	17.0	14.51	9.9	798.61
81A-MH	505.0	11	16.0	13.31	9.08	798.61
81A-ML	505.0	8	16.0	13.31	9.08	798.61
81A-SH	459.5	11	14.0	12.11	8.26	798.61
81A-SL	459.5	8	14.0	12.11	8.26	798.61
81B-LH	550.5	11	17.0	14.51	9.9	1355.32
81B-LL	550.5	8	17.0	14.51	9.9	1355.32
81B-MH	505.0	11	16.0	13.31	9.08	1355.32
81B-ML	505.0	8	16.0	13.31	9.08	1355.32
81B-SH	459.5	11	14.0	12.11	8.26	1355.32
81B-SL	459.5	8	14.0	12.11	8.26	1355.32
81C-LH	550.5	11	17.0	14.51	9.9	1427.12

81C-LL	550.5	8	17.0	14.51	9.9	1427.12
81C-MH	505.0	11	16.0	13.31	9.08	1427.12
81C-ML	505.0	8	16.0	13.31	9.08	1427.12
81C-SH	459.5	11	14.0	12.11	8.26	1427.12
81C-SL	459.5	8	14.0	12.11	8.26	1427.12
81D-LH	550.5	11	17.0	14.51	9.9	303.54
81D-LL	550.5	8	17.0	14.51	9.9	303.54
81D-MH	505.0	11	16.0	13.31	9.08	303.54
81D-ML	505.0	8	16.0	13.31	9.08	303.54
81D-SH	459.5	11	14.0	12.11	8.26	303.54
81D-SL	459.5	8	14.0	12.11	8.26	303.54
82A-LH	550.5	11	17.0	14.51	9.9	1202.98
82A-LL	550.5	8	17.0	14.51	9.9	1202.98
82A-MH	505.0	11	16.0	13.31	9.08	1202.98
82A-ML	505.0	8	16.0	13.31	9.08	1202.98
82A-SH	459.5	11	14.0	12.11	8.26	1202.98
82A-SL	459.5	8	14.0	12.11	8.26	1202.98
82B-LH	580.5	11	6.80	5.80	3.96	1646.08
82B-LL	580.5	8	6.80	5.80	3.96	1646.08
82B-MH	535.0	11	6.30	5.32	3.63	1646.08
82B-ML	535.0	8	6.30	5.32	3.63	1646.08
82B-SH	489.5	11	5.80	4.90	3.34	1646.08
82B-SL	489.5	8	5.80	4.90	3.34	1646.08
83A-LH	580.5	11	6.80	5.80	3.96	1541.50
83A-LL	580.5	8	6.80	5.80	3.96	1541.50
83A-MH	535.0	11	6.30	5.32	3.63	1541.50
83A-ML	535.0	8	6.30	5.32	3.63	1541.50
83A-SH	489.5	11	5.80	4.90	3.34	1541.50
83A-SL	489.5	8	5.80	4.90	3.34	1541.50

83B-LH	580.5	11	6.80	5.80	3.96	1316.39
83B-LL	580.5	8	6.80	5.80	3.96	1316.39
83B-MH	535.0	11	6.30	5.32	3.63	1316.39
83B-ML	535.0	8	6.30	5.32	3.63	1316.39
83B-SH	489.5	11	5.80	4.90	3.34	1316.39
83B-SL	489.5	8	5.80	4.90	3.34	1316.39
83C-LH	580.5	11	6.80	5.80	3.96	1337.47
83C-LL	580.5	8	6.80	5.80	3.96	1337.47
83C-MH	535.0	11	6.30	5.32	3.63	1337.47
83C-ML	535.0	8	6.30	5.32	3.63	1337.47
83C-SH	489.5	11	5.80	4.90	3.34	1337.47
83C-SL	489.5	8	5.80	4.90	3.34	1337.47
83D-LH	580.5	11	6.80	5.80	3.96	1502.32
83D-LL	580.5	8	6.80	5.80	3.96	1502.32
83D-MH	535.0	11	6.30	5.32	3.63	1502.32
83D-ML	535.0	8	6.30	5.32	3.63	1502.32
83D-SH	489.5	11	5.80	4.90	3.34	1502.32
83D-SL	489.5	8	5.80	4.90	3.34	1502.32
83E-LH	580.5	11	6.80	5.80	3.96	1486.57
83E-LL	580.5	8	6.80	5.	3.96	1486.57
83E-MH	535.0	11	6.30	5.32	3.63	1486.57
83E-ML	535.0	8	6.30	5.32	3.63	1486.57
83E-SH	489.5	11	5.80	4.90	3.34	1486.57
83E-SL	489.5	8	5.80	4.90	3.34	1486.57
84A-LH	580.5	11	6.80	5.80	3.96	2037.81
84A-LL	580.5	8	6.80	5.80	3.96	2037.81
84A-MH	535.0	11	6.30	5.32	3.63	2037.81
84A-ML	535.0	8	6.30	5.32	3.63	2037.81
84A-SH	489.5	11	5.80	4.90	3.34	2037.81

84A-SL	489.5	8	5.80	4.90	3.34	2037.81
84B-LH	580.5	11	6.80	5.80	3.96	1851.07
84B-LL	580.5	8	6.80	5.80	3.96	1851.07
84B-MH	535.0	11	6.30	5.32	3.63	1851.07
84B-ML	535.0	8	6.30	5.32	3.63	1851.07
84B-SH	489.5	11	5.80	4.90	3.34	1851.07
84B-SL	489.5	8	5.80	4.90	3.34	1851.07
84C-LH	580.5	11	6.80	5.80	3.96	1941.66
84C-LL	580.5	8	6.80	5.80	3.96	1941.66
84C-MH	535.0	11	6.30	5.32	3.63	1941.66
84C-ML	535.0	8	6.30	5.32	3.63	1941.66
84C-SH	489.5	11	5.80	4.90	3.34	1941.66
84C-SL	489.5	8	5.80	4.90	3.34	1941.66
85-LH	580.5	11	6.80	5.80	3.96	2055.90
85-LL	580.5	8	6.80	5.80	3.96	2055.90
85-MH	535.0	11	6.30	5.32	3.63	2055.90
85-ML	535.0	8	6.30	5.32	3.63	2055.90
85-SH	489.5	11	5.80	4.90	3.34	2055.90
85-SL	489.5	8	5.80	4.90	3.34	2055.90
86A-LH	580.5	11	6.80	5.80	3.96	2138.97
86A-LL	580.5	8	6.80	5.80	3.96	2138.97
86A-MH	535.0	11	6.30	5.32	3.63	2138.97
86A-ML	535.0	8	6.30	5.32	3.63	2138.97
86A-SH	489.5	11	5.80	4.90	3.34	2138.97
86A-SL	489.5	8	5.80	4.90	3.34	2138.97
86B-LH	580.5	11	6.80	5.80	3.96	2213.45
86B-LL	580.5	8	6.80	5.80	3.96	2213.45
86B-MH	535.0	11	6.30	5.32	3.63	2213.45
86B-ML	535.0	8	6.30	5.32	3.63	2213.45

86B-SH	489.5	11	5.80	4.90	3.34	2213.45
86B-SL	489.5	8	5.80	4.90	3.34	2213.45
87A-LH	580.5	11	6.80	5.80	3.96	1982.85
87A-LL	580.5	8	6.80	5.80	3.96	1982.85
87A-MH	535.0	11	6.30	5.32	3.63	1982.85
87A-ML	535.0	8	6.30	5.32	3.63	1982.85
87A-SH	489.5	11	5.80	4.90	3.34	1982.85
87A-SL	489.5	8	5.80	4.90	3.34	1982.85
87B-LH	582.5	11	2.60	2.24	1.53	2008.45
87B-LL	582.5	8	2.60	2.24	1.53	2008.45
87B-MH	537.0	11	2.40	2.07	1.41	2008.45
87B-ML	537.0	8	2.40	2.07	1.41	2008.45
87B-SH	491.5	11	2.20	1.89	1.29	2008.45
87B-SL	491.5	8	2.20	1.89	1.29	2008.45

LL-large body weight, low lactation, LH- large body weight, high lactation, ML- moderate body weight, low lactation, MH-moderate body weight, high lactation, SL- small body weight, low lactation, SH- small body weight, high lactation

Table 3.2a

Net energy maintenance estimates of grazed forages for each month for each Major Land Resource Area (megacalories per kilogram of dry matter)

MLRA	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
102A	1.48	1.48	1.48	1.48	1.63	1.63	1.51	1.48	1.44	1.47	1.48	1.48
102B	1.49	1.49	1.49	1.49	1.68	1.67	1.52	1.50	1.45	1.49	1.49	1.49
102C	1.31	1.31	1.31	1.31	1.49	1.45	1.44	1.37	1.34	1.30	1.31	1.31
106	1.31	1.31	1.31	1.31	1.49	1.45	1.44	1.37	1.34	1.30	1.31	1.31
112	1.61	1.61	1.61	1.61	1.64	1.63	1.58	1.57	1.60	1.60	1.61	1.61
116A	1.85	1.85	1.85	1.85	1.73	1.78	1.70	1.71	1.73	1.83	1.85	1.85
116B	1.92	1.92	1.92	1.92	1.75	1.81	1.73	1.75	1.78	1.89	1.92	1.92
117	1.79	1.79	1.79	1.79	1.70	1.74	1.67	1.67	1.69	1.77	1.79	1.79
118A	1.42	1.42	1.42	1.42	1.55	1.55	1.48	1.46	1.45	1.42	1.42	1.42
118B	1.34	1.34	1.34	1.34	1.53	1.5	1.46	1.41	1.38	1.34	1.34	1.34
119	1.30	1.30	1.30	1.30	1.40	1.38	1.36	1.33	1.32	1.30	1.30	1.30
133B	1.25	1.25	1.25	1.25	1.45	1.44	1.38	1.33	1.30	1.26	1.25	1.25
135B	1.20	1.20	1.20	1.20	1.39	1.38	1.32	1.27	1.24	1.20	1.20	1.20
150A	1.29	1.29	1.29	1.29	1.49	1.48	1.39	1.36	1.35	1.29	1.29	1.29
150B	1.35	1.35	1.35	1.35	1.43	1.44	1.42	1.42	1.42	1.42	1.35	1.35
152B	1.18	1.18	1.18	1.18	1.37	1.37	1.32	1.26	1.23	1.18	1.18	1.18
42	1.13	1.13	1.13	1.13	1.17	1.14	1.16	1.16	1.16	1.13	1.13	1.13
53A	1.45	1.45	1.45	1.45	1.69	1.63	1.52	1.48	1.43	1.45	1.45	1.45
53B	1.47	1.47	1.47	1.47	1.69	1.63	1.51	1.48	1.43	1.46	1.47	1.47
53C	1.32	1.32	1.32	1.32	1.64	1.56	1.48	1.41	1.35	1.32	1.32	1.32
54	1.20	1.20	1.20	1.20	1.72	1.58	1.44	1.37	1.28	1.20	1.20	1.20
55A	1.34	1.34	1.34	1.34	1.57	1.52	1.47	1.40	1.36	1.34	1.34	1.34
55B	1.44	1.44	1.44	1.44	1.70	1.64	1.53	1.49	1.43	1.43	1.44	1.44
55C	1.47	1.47	1.47	1.47	1.71	1.68	1.53	1.5	1.44	1.47	1.47	1.47
56	1.37	1.37	1.37	1.37	1.52	1.48	1.43	1.40	1.40	1.37	1.37	1.37
58C	1.21	1.21	1.21	1.21	1.65	1.54	1.43	1.35	1.29	1.22	1.21	1.21

58D	1.25	1.25	1.25	1.25	1.59	1.50	1.45	1.37	1.33	1.26	1.25	1.25
60A	1.21	1.21	1.21	1.21	1.64	1.51	1.44	1.35	1.28	1.21	1.21	1.21
61	1.23	1.23	1.23	1.23	1.58	1.50	1.43	1.36	1.30	1.23	1.23	1.23
62	1.23	1.23	1.23	1.23	1.58	1.50	1.43	1.36	1.30	1.23	1.23	1.23
63A	1.21	1.21	1.21	1.21	1.60	1.48	1.44	1.35	1.29	1.21	1.21	1.21
63B	1.20	1.20	1.20	1.20	1.66	1.55	1.44	1.36	1.28	1.20	1.20	1.20
64	1.23	1.23	1.23	1.23	1.58	1.48	1.43	1.36	1.32	1.24	1.23	1.23
65	1.28	1.28	1.28	1.28	1.44	1.40	1.41	1.35	1.35	1.28	1.28	1.28
66	1.25	1.25	1.25	1.25	1.53	1.45	1.42	1.35	1.32	1.25	1.25	1.25
67A	1.24	1.24	1.24	1.24	1.52	1.44	1.41	1.34	1.31	1.24	1.24	1.24
70A	1.22	1.22	1.22	1.22	1.43	1.37	1.37	1.29	1.26	1.22	1.22	1.22
70B	1.24	1.24	1.24	1.24	1.33	1.29	1.34	1.28	1.29	1.24	1.24	1.24
71	1.25	1.25	1.25	1.25	1.48	1.43	1.42	1.34	1.30	1.25	1.25	1.25
72	1.23	1.23	1.23	1.23	1.47	1.40	1.40	1.32	1.29	1.23	1.23	1.23
73	1.24	1.24	1.24	1.24	1.48	1.41	1.42	1.33	1.29	1.24	1.24	1.24
74	1.17	1.17	1.17	1.17	1.39	1.37	1.35	1.27	1.24	1.18	1.17	1.17
75	1.25	1.25	1.25	1.25	1.45	1.41	1.41	1.34	1.29	1.25	1.25	1.25
76	1.20	1.20	1.20	1.20	1.41	1.40	1.37	1.30	1.25	1.20	1.20	1.20
77A	1.24	1.24	1.24	1.24	1.54	1.44	1.44	1.33	1.30	1.24	1.24	1.24
77B	1.28	1.28	1.28	1.28	1.46	1.41	1.45	1.34	1.33	1.28	1.28	1.28
77C	1.24	1.24	1.24	1.24	1.43	1.38	1.39	1.31	1.29	1.24	1.24	1.24
77D	1.27	1.27	1.27	1.27	1.34	1.29	1.34	1.33	1.32	1.27	1.27	1.27
77E	1.26	1.26	1.26	1.26	1.48	1.41	1.42	1.34	1.31	1.26	1.26	1.26
78A	1.27	1.27	1.27	1.27	1.45	1.40	1.41	1.33	1.31	1.27	1.27	1.27
78B	1.30	1.30	1.30	1.30	1.41	1.40	1.44	1.35	1.35	1.30	1.30	1.30
78C	1.28	1.28	1.28	1.28	1.45	1.39	1.41	1.33	1.32	1.28	1.28	1.28
79	1.00	1.00	1.00	1.00	1.17	1.15	1.15	1.08	1.06	1.01	1.00	1.00
80A	1.27	1.27	1.27	1.27	1.47	1.41	1.41	1.34	1.32	1.27	1.27	1.27
80B	1.25	1.25	1.25	1.25	1.45	1.40	1.41	1.33	1.29	1.25	1.25	1.25

81A	1.28	1.28	1.28	1.28	1.40	1.36	1.41	1.31	1.31	1.28	1.28	1.28
81B	1.28	1.28	1.28	1.28	1.40	1.36	1.41	1.31	1.31	1.28	1.28	1.28
81C	1.16	1.16	1.16	1.16	1.35	1.36	1.33	1.25	1.21	1.16	1.16	1.16
81D	1.10	1.10	1.10	1.10	1.14	1.08	1.10	1.24	1.18	1.09	1.10	1.10
82A	1.27	1.27	1.27	1.27	1.41	1.42	1.42	1.33	1.30	1.27	1.27	1.27
82B	1.27	1.27	1.27	1.27	1.46	1.40	1.41	1.34	1.32	1.27	1.27	1.27
83A	1.21	1.21	1.21	1.21	1.39	1.40	1.34	1.28	1.25	1.21	1.21	1.21
83B	1.26	1.26	1.26	1.26	1.43	1.41	1.41	1.33	1.29	1.26	1.26	1.26
83C	1.27	1.27	1.27	1.27	1.48	1.43	1.39	1.33	1.31	1.26	1.27	1.27
83D	1.28	1.28	1.28	1.28	1.50	1.46	1.40	1.35	1.33	1.28	1.28	1.28
83E	1.26	1.26	1.26	1.26	1.52	1.43	1.36	1.32	1.31	1.26	1.26	1.26
84A	1.18	1.18	1.18	1.18	1.40	1.38	1.34	1.27	1.23	1.18	1.18	1.18
84B	1.05	1.05	1.05	1.05	1.22	1.18	1.18	1.12	1.09	1.05	1.05	1.05
84C	1.20	1.20	1.20	1.20	1.41	1.40	1.34	1.29	1.24	1.20	1.20	1.20
85	1.12	1.12	1.12	1.12	1.31	1.27	1.26	1.20	1.16	1.12	1.12	1.12
86A	1.16	1.16	1.16	1.16	1.35	1.38	1.30	1.24	1.21	1.16	1.16	1.16
86B	1.27	1.27	1.27	1.27	1.46	1.45	1.33	1.32	1.30	1.27	1.27	1.27
87A	1.25	1.25	1.25	1.25	1.44	1.43	1.34	1.31	1.28	1.25	1.25	1.25
87B	1.22	1.22	1.22	1.22	1.41	1.43	1.31	1.28	1.26	1.22	1.22	1.22

Table 3.3b

Net energy gain estimates of grazed forages for each month for each Major Land Resource Area (megacalories per kilogram of dry matter)

MLRA	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
102A	0.69	0.69	0.69	0.69	0.91	0.91	0.79	0.76	0.72	0.75	0.69	0.69
102B	0.75	0.75	0.75	0.75	0.96	0.95	0.8	0.78	0.73	0.77	0.75	0.75
102C	0.44	0.44	0.44	0.44	0.77	0.73	0.72	0.65	0.62	0.58	0.44	0.44
106	0.43	0.43	0.43	0.43	0.77	0.73	0.72	0.65	0.62	0.58	0.43	0.43
112	0.83	0.83	0.83	0.83	0.92	0.91	0.86	0.85	0.88	0.88	0.83	0.83
116A	1.11	1.11	1.11	1.11	1.01	1.05	0.98	0.99	1.01	1.11	1.11	1.11
116B	1.20	1.20	1.20	1.20	1.04	1.09	1.01	1.03	1.06	1.17	1.20	1.20
117	1.02	1.02	1.02	1.02	0.98	1.02	0.94	0.95	0.97	1.05	1.02	1.02
118A	0.72	0.72	0.72	0.72	0.85	0.85	0.78	0.76	0.75	0.72	0.72	0.72
118B	0.55	0.55	0.55	0.55	0.81	0.78	0.74	0.69	0.66	0.62	0.55	0.55
119	0.63	0.63	0.63	0.63	0.73	0.72	0.69	0.66	0.65	0.63	0.63	0.63
133B	0.53	0.53	0.53	0.53	0.76	0.74	0.69	0.64	0.61	0.56	0.53	0.53
135B	0.47	0.47	0.47	0.47	0.71	0.7	0.64	0.59	0.56	0.52	0.47	0.47
150A	0.57	0.57	0.57	0.57	0.79	0.78	0.70	0.67	0.65	0.59	0.57	0.57
150B	0.63	0.63	0.63	0.63	0.71	0.72	0.70	0.70	0.70	0.69	0.63	0.63
152B	0.46	0.46	0.46	0.46	0.72	0.73	0.67	0.61	0.58	0.53	0.46	0.46
42	0.46	0.46	0.46	0.46	0.49	0.46	0.48	0.49	0.49	0.46	0.46	0.46
53A	0.73	0.73	0.73	0.73	0.97	0.91	0.8	0.76	0.71	0.73	0.73	0.73
53B	0.75	0.75	0.75	0.75	0.97	0.91	0.79	0.76	0.71	0.74	0.75	0.75
53C	0.53	0.53	0.53	0.53	0.92	0.84	0.76	0.69	0.63	0.59	0.53	0.53
54	0.48	0.48	0.48	0.48	1.00	0.86	0.72	0.65	0.56	0.48	0.48	0.48
55A	0.62	0.62	0.62	0.62	0.85	0.80	0.74	0.68	0.64	0.62	0.62	0.62
55B	0.72	0.72	0.72	0.72	0.97	0.92	0.80	0.76	0.71	0.71	0.72	0.72
55C	0.75	0.75	0.75	0.75	0.99	0.96	0.80	0.78	0.72	0.74	0.75	0.75
56	0.66	0.66	0.66	0.66	0.81	0.77	0.73	0.69	0.69	0.66	0.66	0.66
58C	0.49	0.49	0.49	0.49	0.92	0.82	0.71	0.63	0.57	0.50	0.49	0.49
58D	0.53	0.53	0.53	0.53	0.87	0.78	0.73	0.65	0.61	0.54	0.53	0.53
60A	0.49	0.49	0.49	0.49	0.92	0.79	0.72	0.63	0.56	0.49	0.49	0.49
61	0.51	0.51	0.51	0.51	0.86	0.78	0.71	0.63	0.58	0.51	0.51	0.51
62	0.51	0.51	0.51	0.51	0.86	0.78	0.71	0.63	0.58	0.51	0.51	0.51
63A	0.49	0.49	0.49	0.49	0.88	0.76	0.72	0.63	0.57	0.49	0.49	0.49
63B	0.48	0.48	0.48	0.48	0.94	0.83	0.72	0.63	0.56	0.48	0.48	0.48
64	0.51	0.51	0.51	0.51	0.86	0.76	0.71	0.64	0.60	0.52	0.51	0.51
65	0.56	0.56	0.56	0.56	0.72	0.68	0.69	0.63	0.63	0.56	0.56	0.56
66	0.53	0.53	0.53	0.53	0.81	0.73	0.70	0.63	0.6	0.53	0.53	0.53
67A	0.52	0.52	0.52	0.52	0.81	0.72	0.70	0.63	0.59	0.52	0.52	0.52
70A	0.52	0.52	0.52	0.52	0.74	0.67	0.68	0.59	0.57	0.52	0.52	0.52
70B	0.54	0.54	0.54	0.54	0.63	0.59	0.64	0.59	0.59	0.54	0.54	0.54
71	0.53	0.53	0.53	0.53	0.76	0.71	0.70	0.61	0.58	0.53	0.53	0.53
72	0.52	0.52	0.52	0.52	0.76	0.69	0.69	0.61	0.58	0.52	0.52	0.52
73	0.52	0.52	0.52	0.52	0.76	0.69	0.69	0.61	0.57	0.52	0.52	0.52

74	0.52	0.52	0.52	0.52	0.73	0.71	0.69	0.61	0.58	0.52	0.52	0.52
75	0.53	0.53	0.53	0.53	0.73	0.69	0.69	0.61	0.57	0.53	0.53	0.53
76	0.52	0.52	0.52	0.52	0.74	0.72	0.70	0.62	0.58	0.53	0.52	0.52
77A	0.52	0.52	0.52	0.52	0.82	0.72	0.72	0.61	0.58	0.52	0.52	0.52
77B	0.56	0.56	0.56	0.56	0.74	0.68	0.72	0.62	0.61	0.56	0.56	0.56
77C	0.54	0.54	0.54	0.54	0.74	0.68	0.69	0.61	0.59	0.54	0.54	0.54
77D	0.54	0.54	0.54	0.54	0.62	0.57	0.62	0.60	0.60	0.54	0.54	0.54
77E	0.54	0.54	0.54	0.54	0.76	0.69	0.70	0.61	0.59	0.54	0.54	0.54
78A	0.49	0.49	0.49	0.49	0.73	0.68	0.69	0.61	0.59	0.54	0.49	0.49
78B	0.58	0.58	0.58	0.58	0.69	0.68	0.72	0.63	0.63	0.58	0.58	0.58
78C	0.56	0.56	0.56	0.56	0.73	0.67	0.69	0.61	0.60	0.56	0.56	0.56
79	0.32	0.32	0.32	0.32	0.61	0.59	0.59	0.52	0.50	0.45	0.32	0.32
80A	0.42	0.42	0.42	0.42	0.75	0.69	0.69	0.62	0.60	0.55	0.42	0.42
80B	0.43	0.43	0.43	0.43	0.73	0.68	0.68	0.61	0.57	0.53	0.43	0.43
81A	0.56	0.56	0.56	0.56	0.68	0.64	0.69	0.59	0.59	0.56	0.56	0.56
81B	0.56	0.56	0.56	0.56	0.68	0.64	0.69	0.59	0.59	0.56	0.56	0.56
81C	0.43	0.43	0.43	0.43	0.71	0.71	0.68	0.6	0.56	0.51	0.43	0.43
81D	0.38	0.38	0.38	0.38	0.42	0.35	0.37	0.52	0.46	0.37	0.38	0.38
82A	0.55	0.55	0.55	0.55	0.69	0.70	0.69	0.61	0.58	0.55	0.55	0.55
82B	0.49	0.49	0.49	0.49	0.74	0.68	0.69	0.62	0.60	0.55	0.49	0.49
83A	0.48	0.48	0.48	0.48	0.71	0.71	0.66	0.60	0.56	0.52	0.48	0.48
83B	0.54	0.54	0.54	0.54	0.71	0.69	0.69	0.61	0.57	0.54	0.54	0.54
83C	0.54	0.54	0.54	0.54	0.76	0.71	0.67	0.61	0.59	0.54	0.54	0.54
83D	0.56	0.56	0.56	0.56	0.78	0.74	0.67	0.63	0.61	0.56	0.56	0.56
83E	0.54	0.54	0.54	0.54	0.8	0.71	0.64	0.60	0.58	0.54	0.54	0.54
84A	0.39	0.39	0.39	0.39	0.73	0.72	0.67	0.61	0.56	0.52	0.39	0.39
84B	0.38	0.38	0.38	0.38	0.61	0.58	0.57	0.51	0.48	0.45	0.38	0.38
84C	0.44	0.44	0.44	0.44	0.73	0.72	0.67	0.61	0.57	0.53	0.44	0.44
85	0.38	0.38	0.38	0.38	0.66	0.62	0.61	0.55	0.51	0.47	0.38	0.38
86A	0.44	0.44	0.44	0.44	0.70	0.73	0.65	0.59	0.56	0.52	0.44	0.44
86B	0.55	0.55	0.55	0.55	0.74	0.73	0.61	0.60	0.58	0.55	0.55	0.55
87A	0.54	0.54	0.54	0.54	0.72	0.71	0.62	0.59	0.57	0.54	0.54	0.54
87B	0.50	0.50	0.50	0.50	0.72	0.73	0.62	0.59	0.57	0.53	0.50	0.50

Table 3.3

Diet formulations with net energy estimates of supplemental and delivered rations for each diet region

		Supplement (summer months)	**Delivered Ration (winter months)**
North	*East*	88% smooth brome hay 9% whole grain corn 3% corn dry distillers' grain with solubles *Net energy maintenance: 1.4311 Mcal/kg DM* *Net energy gain: 0.8388 Mcal/kg DM*	88% smooth brome hay 9% whole grain corn 3% corn dry distillers' grain with solubles *Net energy maintenance: 1.4311 Mcal/kg DM* *Net energy gain: 0.8388 Mcal/kg DM*
	West	82% prairie hay 18% alfalfa *Net energy maintenance: 1.0422 Mcal/kg DM* *Net energy gain: 04886 Mcal/kg DM*	82% prairie hay 18% alfalfa *Net energy maintenance: 1.0422 Mcal/kg DM* *Net energy gain: 04886 Mcal/kg DM*
Central	*East*	88% smooth brome hay 9% whole grain corn 3% corn dry distillers' grain with solubles *Net energy maintenance: 1.4311 Mcal/kg DM* *Net energy gain: 0.8388 Mcal/kg DM*	88% smooth brome hay 9% whole grain corn 3% corn dry distillers' grain with solubles *Net energy maintenance: 1.4311 Mcal/kg DM* *Net energy gain: 0.838 Mcal/kg DM*
	West	93% prairie hay 7% corn dry distillers' grain with solubles *Net energy maintenance: 1.0754 Mcal/kg DM* *Net energy gain: 0.5156 Mcal/kg DM*	82% prairie hay 18% alfalfa *Net energy maintenance: 1.0422 Mcal/kg DM Net energy gain: 04886 Mcal/kg DM*
South	*East*	88% bermuda hay 12% corn dry distillers' grain with solubles *Net energy maintenance: 0.89 Mcal/kg DM Net energy gain: 0.3408*	88% bermuda hay 12% corn dry distillers' grain with solubles *Net energy maintenance: 0.89 Mcal/kg DM* *Net energy gain: 0.3408*
	West	93% prairie hay 7% corn dry distillers' grain with solubles *Net energy maintenance: 1.0754 Mcal/kg DM* *Net energy gain: 0.5156 Mcal/kg DM*	88% prairie hay 12% corn dry distillers' grain with solubles *Net energy maintenance: 1.1364 Mcal/kg DM* *Net energy gain: 0.5696 Mcal/kg DM*

Table 3.4

Monthly water requirements of crops in the Great Plains (millimeters)

					Corn				
	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov
North Dakota	-	-	14.4	25.05	34.5	34.5	4.899	-	-
South Dakota	-	-	14.4	25.05	34.5	34.5	4.899	-	-
Nebraska	-	1.2	17.1	26.79	34.5	21.9	1.401	-	-
Kansas	-	6	21.99	30.99	30.45	19.599	-	-	-
Oklahoma	-	7.2	23.199	32.049	28.398	-	-	-	-
Texas	9.6	24	33.45	26.85	9.099	-	-	-	-
					Sorghum				
	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov
North Dakota	-	-	3.48	26	33	19.95	1.3	-	-
South Dakota	-	-	3.48	26	33	19.95	1.3	-	-
Nebraska	-	-	4.9	20.5	30.9	26.7	11.05	-	-
Kansas	-	-	5.25	20.9	31.26	26.25	10.4	-	-
Oklahoma	-	-	6.3	22.5	31.95	25.8	9	-	-
Texas	12.35	22.1	32.3	24.7	-	-	-	-	-
					Alfalfa				
	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov
North Dakota	-	-	31.5	31.5	31.5	31.5	6.3	-	-
South Dakota	-	11.55	31.5	31.5	31.5	31.5	21	-	-

Nebraska	-	22.05	31.5	31.5	31.5	31.5	31.5	1.05	-
Kansas	-	31.5	31.5	31.5	31.5	31.5	31.5	31.5	1.05
Oklahoma	21	31.5	31.5	31.5	31.5	31.5	31.5	13.65	-
Texas	26.25	31.5	31.5	31.5	31.5	31.5	21	-	-

Table 3.5a

Annual resource of all genetic potentials fed corn diets across the Great Plains scaled by the average kilograms of weaning weight produced

Genetic Potential	Large weight, high lactation	Large weight, low lactation	Moderate weight, high lactation	Moderate weight, low lactation	Small weight, high lactation	Small weight, low lactation
Crop Land (ha/kg WW)	0.00222	0.00215	0.00220	0.00213	0.00217	0.00210
Grazing Land (ha/kg WW)	0.0225	0.0240	0.0211	0.0226	0.0197	0.0211
Total Land (ha/kg WW)	0.0245	0.0260	0.0231	0.0245	0.0217	0.0230
Irrigation Water (liters/kg WW)	994	972	980	955	964	940
Drinking Water (liters/kg WW)	55.4	57.0	54.3	55.9	53.2	54.8
Blue Water (liters/kg WW)	1049	1027	1034	1012	1018	998
Nitrogen Fertilizer (kg/yr/kg WW)	0.913	0.966	0.862	0.912	0.811	0.859
Phosphorus (kg/yr/kg WW)	21.7	21.4	21.2	20.9	20.6	20.4
Potassium (kg/yr/kg WW)	62.1	61.0	60.7	59.6	59.2	58.4
Methane (kg/kg WW)	0.301	0.312	0.294	0.302	0.285	0.292

Table 3.6b

Annual resource of all genetic potentials fed sorghum diets across the Great Plains scaled by the average kilograms of weaning weight produced

Genetic Potential	Large weight, high lactation	Large weight, low lactation	Moderate weight, high lactation	Moderate weight, low lactation	Small weight, high lactation	Small weight, low lactation
Crop Land (ha/kg WW)	0.00229	0.00222	0.00227	0.00219	0.00224	0.00217
Grazing Land (ha/kg WW)	0.0225	0.0240	0.0211	0.0226	0.0197	0.0211
Total Land (ha/kg WW)	0.0246	0.0261	0.0232	0.0246	0.0218	0.0231
Irrigation Water (liters/kg WW)	1409	1382	1392	1360	1370	1338
Drinking Water (liters/kg WW)	55.4	57.0	54.3	55.9	53.2	54.8
Blue Water (liters/kg WW)	1461	1438	1445	1417	1425	1397
Nitrogen Fertilizer (kg/yr/kg WW)	0.913	0.965	0.861	0.912	0.810	0.858
Phosphorus (kg/yr/kg WW)	21.7	21.4	21.2	20.9	20.6	20.4
Potassium (kg/yr/kg WW)	62.1	61.0	60.7	59.6	59.2	58.4
Methane (kg/kg WW)	0.302	0.313	0.295	0.303	0.286	0.292

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Chapter 1

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Appendix A - Additional Tables

Table A.1

Forage species used to represent native range and cultivated pasture in each MLRA

MLRA	Range Species	Pasture Species
102A	Kentucky bluegrass smooth brome little bluestem big bluestem	Kentucky bluegrass smooth brome western wheatgrass
102B	Kentucky bluegrass smooth brome little bluestem big bluestem	Kentucky bluegrass smooth brome western wheatgrass
102C	big bluestem little bluestem sideoats grama Indiangrass switchgrass	Kentucky bluegrass smooth brome white clover tall fescue sedge
106	big bluestem little bluestem Indiangrass sideoats grama switchgrass	Kentucky bluegrass smooth brome white clover tall fescue sedge

112	big bluestem little bluestem Indiangrass switchgrass	white clover tall fescue Kentucky bluegrass orchardgrass
116A	*assumed to be the same forage composition as 112 range big bluestem little bluestem Indiangrass switchgrass	white clover tall fescue Kentucky bluegrass orchardgrass
116B	*assumed to be the same forage composition as 112 range big bluestem little bluestem Indiangrass switchgrass	white clover tall fescue Kentucky bluegrass orchardgrass
117	*assumed to be the same forage composition as 112 range big bluestem little bluestem Indiangrass switchgrass	white clover tall fescue Kentucky bluegrass orchardgrass
118A	alkali sacaton blue grama sideoats grama	*assumed to have same forage composition as 117 pasture bermudagrass bahiagrass dallisgrass white clover
118B	little bluestem big bluestem indiangrass switchgrass	*assumed to have same forage composition as 117 pasture bermudagrass

		bahiagrass dallisgrass white clover
119	*assumed to be the same forage composition as 118B range little bluestem big bluestem Indiangrass switchgrass	bermudagrass bahiagrass dallisgrass white clover
133B	*assumed to be combination of 87A and 150A range forage composition little bluestem switchgrass big bluestem Indiangrass eastern gamagrass Florida paspalum	bermudagrass bahiagrass sedge dallisgrass
135B	*assumed to be a combination of 85, 86A, 87A, and 150A range forage composition little bluestem switchgrass big bluestem Indiangrass eastern gamagrass Florida paspalum	bermudagrass bahiagrass sedge dallisgrass
150A	little bluestem switchgrass big bluestem Indiangrass eastern gamagrass Florida paspalum	*assumed to have the same forage composition as 133B pasture bermudagrass bahiagrass sedge dallisgrass
150B	saltmeadow cordgrass smooth cordgrass seashore dropseed little bluestem	*assumed to have the same forage composition as 133B pasture bermudagrass bahiagrass sedge

		dallisgrass
152B	*assumed forage composition was the same as 150B range saltmeadow cordgrass smooth cordgrass seashore dropseed little bluestem	bermudagrass bahiagrass sedge dallisgrass
42	alkali sacaton big sacaton black grama tobosagrass blue grama sideoats grama	* assumed to have the same forage composition as 81A pasture yellow bluestem smooth brome cheatgrass crested wheatgrass
53A	western wheatgrass green needlegrass little bluestem	Kentucky bluegrass smooth brome western wheatgrass
53B	western wheatgrass Kentucky bluegrass	smooth brome Kentucky bluegrass crested wheatgrass blue grama
53C	western wheatgrass blue grama smooth brome big bluestem Kentucky bluegrass	smooth brome Kentucky bluegrass crested wheatgrass blue grama
54	western wheatgrass	smooth brome crested wheatgrass Kentucky bluegrass western wheatgrass blue grama
55A	*assumed to be a combination of 53B, 55B, and 56 range forage composition big bluestem western wheatgrass little bluestem sideoats grama blue grama	Kentucky bluegrass smooth brome western wheatgrass

	sand bluestem switchgrass alkali sacaton big bluestem western wheatgrass little bluestem porcupinegrass slender wheatgrass Kentucky bluegrass wooly sedge switchgrass	
55B	big bluestem western wheatgrass little bluestem porcupinegrass slender wheatgrass	Kentucky bluegrass smooth brome western wheatgrass
55C	western wheatgrass Kentucky bluegrass smooth brome	smooth brome Kentucky bluegrass crested wheatgrass blue grama
56	big bluestem Indiangrass little bluestem woolly sedge switchgrass	Kentucky bluegrass reed canarygrass smooth brome timothy red clover
58C	western wheatgrass green needlegrass needle and thread blue grama	smooth brome crested wheatgrass Kentucky bluegrass western wheatgrass blue grama
58D	western wheatgrass blue grama needle and thread	smooth brome crested wheatgrass Kentucky bluegrass western wheatgrass blue grama
60A	western wheatgrass blue grama	smooth brome crested wheatgrass Kentucky bluegrass western wheatgrass blue grama
61	western wheatgrass green needlegrass big bluestem needle and thread blue grama little bluestem	Kentucky bluegrass smooth brome crested wheatgrass cheatgrass western wheatgrass

62	*assumed to be the same forage composition as 61 range western wheatgrass green needlegrass big bluestem needle and thread blue grama little bluestem	Kentucky bluegrass smooth brome crested wheatgrass cheatgrass western wheatgrass
63A	western wheatgrass blue grama big bluestem	smooth brome Kentucky bluegrass crested wheatgrass blue grama
63B	western wheatgrass smooth brome green needlegrass blue grama big bluestem	smooth brome Kentucky bluegrass crested wheatgrass blue grama
64	western wheatgrass blue grama sedge needle and thread big bluestem	smooth brome crested wheatgrass Kentucky bluegrass western wheatgrass blue grama
65	prairie sandreed sand bluestem little bluestem switchgrass needle and thread sedge big bluestem	sedge redtop western wheatgrass prairie sandreed big bluestem
66	western wheatgrass switchgrass big bluestem little bluestem sand bluestem	smooth brome crested wheatgrass Kentucky bluegrass western wheatgrass blue grama
67A	*assumed to be a combination of 64 and 72 range forage composition western wheatgrass big bluestem little bluestem sideoats grama blue grama sand bluestem switchgrass	yellow bluestem smooth brome cheatgrass crested wheatgrass

	alkali sacaton sedge needle and thread	
70A	blue grama western wheatgrass sideoats grama alkali sacaton little bluestem	* assumed to have the same forage compostion as 77C pasute yellow bluestem smooth brome cheatgrass crested wheatgrass
70B	blue grama sideoats grama little bluestem black grama alkali sacaton sand bluestem	* assumed to have the same forage compostion as 77C pasture yellow bluestem smooth brome cheatgrass crested wheatgrass
71	little bluestem big bluestem sideoats grama western wheatgrass blue grama switchgrass	cuman ragweed yellow bluestem bermudagrass sedge
72	big bluestem western wheatgrass little bluestem sideoats grama blue grama sand bluestem switchgrass alkali sacaton	bermudagrass bahiagrass sedge dallisgrass
73	big bluestem little bluestem sideoats grama switchgrass western wheatgrass blue grama Indiangrass	cuman ragweed yellow bluestem Bermudagrass sedge
74	big bluestem little bluestem switchgrass Indiangrass eastern gamagrass sand bluestem	cuman ragweed yellow bluestem bermudagrass sedge

75	big bluestem little bluestem sideoats grama Indiangrass switchgrass	smooth brome sedge Kentucky bluegrass little bluestem
76	big bluestem little bluestem Indiangrass switchgrass eastern gamagrass	Cuman ragweed yellow bluestem Bermudagrass sedge
77A	western wheatgrass blue grama sideoats grama	yellow bluestem smooth brome cheatgrass crested wheatgrass
77B	blue grama sideoats grama little bluestem sand bluestem western wheatgrass	yellow bluestem smooth brome cheatgrass crested wheatgrass
77C	western wheatgrass sideoats grama blue grama little bluestem alkali sacaton sand bluestem	yellow bluestem smooth brome cheatgrass crested wheatgrass
77D	blue grama black grama sideoats grama buffalograss	yellow bluestem smooth brome cheatgrass crested wheatgrass
77E	little bluestem blue grama sideoats grama western wheatgrass switchgrass sand bluestem Indiangrass	yellow bluestem smooth brome cheatgrass crested wheatgrass
78A	*assumed to be an combination of 78C and 80B range forage composition western wheatgrass sideoats grama blue grama	cuman ragweed yellow bluestem bermudagrass sedge

	little bluestem alkali sacaton sand bluestem switchgrass Indiangrass	
78B	little bluestem sideoats grama sand bluestem	cuman ragweed yellow bluestem bermudagrass sedge
78C	switchgrass little bluestem Indiangrass sideoats grama sand bluestem	cuman ragweed yellow bluestem bermudagrass sedge
79	big bluestem switchgrass sand bluestem little bluestem Indiangrass eastern gamagrass	cuman ragweed yellow bluestem bermudagrass sedge
80A	big bluestem little bluestem switchgrass Indiangrass sand bluestem	cuman ragweed yellow bluestem bermudagrass sedge
80B	little bluestem big bluestem Indiangrass sideoats grama switchgrass	cuman ragweed yellow bluestem Bermudagrass sedge
81A	sideoats grama	yellow bluestem smooth brome cheatgrass crested wheatgrass
81B	sideoats grama	*assumed to have the same forage composition as 81A pasture yellow bluestem smooth brome cheatgrass crested wheatgrass
81C	little bluestem Indiangrass big bluestem sideoats grama	bermudagrass dallisgrass sedge

	switchgrass eastern gamagrass	
81D	black grama bush muhly slim tridens	*assumed to have the same forage composition as 81A pasture yellow bluestem smooth brome cheatgrass crested wheatgrass
82A	little bluestem sideoats grama	*assumed to have the same forage composition as 81C pasture bermudagrass dallisgrass sedge
82B	*assumed to be combination of 78C and 80A range forage composition big bluestem little bluestem switchgrass Indiangrass sand bluestem sideoats grama	*assumed to have the same forage composition as 78C pasture cuman ragweed yellow bluestem Bermudagrass sedge
83A	little bluestem	*assumed to have the same forage composition as 86A pasture bermudagrass yellow bluestem sedge
83B	little bluestem Indiangrass	*assumed to have the same forage composition as 86A pasture bermudagrass yellow bluestem sedge
83C	little bluestem Indiangrass	*assumed to have the same forage composition as 86A pasture bermudagrass yellow bluestem sedge

83D	switchgrass little bluestem	*assumed to have the same forage composition as 86A pasture bermudagrass yellow bluestem sedge
83E	switchgrass	*assumed to have the same forage composition as 86A pasture bermudagrass yellow bluestem sedge
84A	big bluestem little bluestem Indiangrass switchgrass eastern gamagrass	bermudagrass dallisgrass sedge
84B	little bluestem Indiangrass switchgrass big bluestem sideoats grama	bermudagrass dallisgrass sedge

Table A.2

Estimates of grazing land, crop land, and total land for corn and sorghum formulated diets for a 100-head cow-calf herd with various genetic potentials for mature weight and peak lactation in the Great Plains (hectares)

MLRA	Grazing Land	Crop land for corn-based diets	Crop land for sorghum-based diets	Total land for corn-based diets	Total land for sorghum-based diets
102A-LL	293.00	75.63	82.65	368.63	375.65
102A-LH	293.00	79.36	86.73	372.36	379.73
102A-ML	263.61	72.46	79.19	336.07	342.80
102A-MH	263.61	76.17	83.24	339.78	346.85
102A-SL	234.08	68.98	75.39	303.06	309.47
102A-SH	234.08	73.23	80.03	307.31	314.11
102B-LL	293.00	57.99	80.46	350.99	373.46
102B-LH	293.00	60.70	84.22	353.70	377.22
102B-ML	263.61	55.60	77.14	319.21	340.75
102B-MH	263.61	55.60	77.14	319.21	340.75
102B-SL	234.08	58.72	81.47	292.80	315.55
102B-SH	234.08	53.34	74.00	287.42	308.08
102C-LL	293.00	56.27	78.07	349.27	371.07
102C-LH	293.00	60.09	63.84	353.09	356.84
102C-ML	263.61	62.82	66.74	326.43	330.35
102C-MH	263.61	57.10	60.67	320.71	324.28
102C-SL	234.08	60.32	64.09	294.40	298.17
102C-SH	234.08	54.18	57.56	288.26	291.64
106-LL	243.26	67.89	69.57	311.15	312.83
106-LH	243.26	72.01	73.79	315.27	317.05
106-ML	224.04	65.93	67.57	289.97	291.61
106-MH	224.04	70.31	72.06	294.35	296.10
106-SL	204.69	63.67	65.25	268.36	269.94
106-SH	204.69	68.08	69.77	272.77	274.46
112-LL	243.26	58.22	60.31	301.48	303.57
112-LH	243.26	60.68	62.85	303.94	306.11
112-ML	224.04	57.08	59.13	281.12	283.17
112-MH	224.04	59.59	61.73	283.63	285.77
112-SL	204.69	55.68	57.67	260.37	262.36

112-SH	204.69	58.37	60.46	263.06	265.15
116A-LL	243.26	59.67	63.83	302.93	307.09
116A-LH	243.26	62.43	66.78	305.69	310.04
116A-ML	224.04	57.92	61.96	281.96	286.00
116A-MH	224.04	61.07	65.33	285.11	289.37
116A-SL	204.69	55.72	59.61	260.41	264.30
116A-SH	204.69	59.47	63.62	264.16	268.31
116B-LL	243.26	66.25	68.47	309.51	311.73
116B-LH	243.26	68.98	71.30	312.24	314.56
116B-ML	224.04	63.99	66.14	288.03	290.18
116B-MH	224.04	67.24	69.49	291.28	293.53
116B-SL	204.69	61.36	63.42	266.05	268.11
116B-SH	204.69	65.35	67.54	270.04	272.23
117-LL	243.26	74.10	84.97	317.36	328.23
117-LH	243.26	78.09	89.54	321.35	332.80
117-ML	224.04	71.74	82.26	295.78	306.30
117-MH	224.04	76.17	87.34	300.21	311.38
117-SL	204.69	69.11	79.25	273.80	283.94
117-SH	204.69	74.32	85.21	279.01	289.90
118A-LL	243.26	69.14	73.14	312.40	316.40
118A-LH	243.26	77.01	81.46	320.27	324.72
118A-ML	224.04	66.69	70.55	290.73	294.59
118A-MH	224.04	74.40	78.70	298.44	302.74
118A-SL	204.69	64.26	67.97	268.95	272.66
118A-SH	204.69	72.18	76.35	276.87	281.04
118B-LL	243.26	61.95	65.71	305.21	308.97
118B-LH	243.26	65.61	69.58	308.87	312.84
118B-ML	224.04	59.89	63.52	283.93	287.56
118B-MH	224.04	63.80	67.66	287.84	291.70
118B-SL	204.69	57.67	61.16	262.36	265.85
118B-SH	204.69	62.35	66.10	267.04	270.79
119-LL	243.26	61.71	66.06	304.97	309.32
119-LH	243.26	76.25	81.62	319.51	324.88
119-ML	224.04	60.76	65.03	284.80	289.07
119-MH	224.04	74.58	79.83	298.62	303.87
119-SL	204.69	60.74	65.02	265.43	269.71
119-SH	204.69	72.07	77.14	276.76	281.83

133B-LL	243.26	58.92	62.37	302.18	305.63
133B-LH	243.26	71.58	75.77	314.84	319.03
133B-ML	224.04	56.97	60.31	281.01	284.35
133B-MH	224.04	68.86	72.89	292.90	296.93
133B-SL	204.69	57.54	60.91	262.23	265.60
133B-SH	204.69	65.85	69.71	270.54	274.40
135B-LL	243.26	53.53	58.59	296.79	301.85
135B-LH	243.26	67.00	73.34	310.26	316.60
135B-ML	224.04	52.89	57.89	276.93	281.93
135B-MH	224.04	65.63	71.84	289.67	295.88
135B-SL	204.69	51.98	56.90	256.67	261.59
135B-SH	204.69	62.66	68.59	267.35	273.28
150A-LL	243.26	46.73	47.66	289.99	290.92
150A-LH	243.26	48.52	49.49	291.78	292.75
150A-ML	224.04	44.16	45.04	268.20	269.08
150A-MH	224.04	47.18	48.12	271.22	272.16
150A-SL	204.69	42.29	43.13	246.98	247.82
150A-SH	204.69	45.96	46.87	250.65	251.56
150B-LL	243.26	49.63	50.19	292.89	293.45
150B-LH	243.26	54.67	55.29	297.93	298.55
150B-ML	224.04	48.25	48.80	272.29	272.84
150B-MH	224.04	53.61	54.22	277.65	278.26
150B-SL	204.69	46.89	47.42	251.58	252.11
150B-SH	204.69	52.32	52.92	257.01	257.61
152B-LL	243.26	57.91	57.82	301.17	301.08
152B-LH	243.26	70.73	70.62	313.99	313.88
152B-ML	224.04	57.15	57.07	281.19	281.11
152B-MH	224.04	68.84	68.73	292.88	292.77
152B-SL	204.69	56.45	56.36	261.14	261.05
152B-SH	204.69	66.23	66.13	270.92	270.82
42-LL	1572.34	38.89	42.13	1611.23	1614.47
42-LH	1572.34	44.54	48.14	1616.88	1620.48
42-ML	1442.47	38.38	41.55	1480.85	1484.02
42-MH	1442.47	43.12	46.58	1485.59	1489.05
42-SL	1312.46	37.13	40.18	1349.59	1352.64
42-SH	1312.46	41.70	45.01	1354.16	1357.47
53A-LL	687.62	65.60	65.60	753.22	753.22

53A-LH	687.62	63.67	63.67	751.29	751.29
53A-ML	630.43	61.77	61.77	692.20	692.20
53A-MH	630.43	59.93	59.93	690.36	690.36
53A-SL	573.37	57.66	57.66	631.03	631.03
53A-SH	573.37	56.70	56.70	630.07	630.07
53B-LL	328.11	96.63	96.63	424.74	424.74
53B-LH	328.11	105.01	105.01	433.12	433.12
53B-ML	304.17	92.46	92.46	396.63	396.63
53B-MH	304.17	101.31	101.31	405.48	405.48
53B-SL	280.10	88.57	88.57	368.67	368.67
53B-SH	280.10	96.94	96.94	377.04	377.04
53C-LL	328.11	92.71	92.71	420.82	420.82
53C-LH	328.11	101.63	101.63	429.74	429.74
53C-ML	304.17	89.21	89.21	393.38	393.38
53C-MH	304.17	98.48	98.48	402.65	402.65
53C-SL	280.10	85.27	85.27	365.37	365.37
53C-SH	280.10	94.88	94.88	374.98	374.98
54-LL	687.62	69.89	69.89	757.51	757.51
54-LH	687.62	76.44	76.44	764.06	764.06
54-ML	630.43	66.69	66.69	697.12	697.12
54-MH	630.43	74.32	74.32	704.75	704.75
54-SL	573.37	64.84	64.84	638.21	638.21
54-SH	573.37	71.81	71.81	645.18	645.18
55A-LL	328.11	74.67	78.52	402.78	406.63
55A-LH	328.11	78.57	82.61	406.68	410.72
55A-ML	304.17	72.31	76.03	376.48	380.20
55A-MH	304.17	76.32	80.25	380.49	384.42
55A-SL	280.10	70.02	73.63	350.12	353.73
55A-SH	280.10	74.23	78.05	354.33	358.15
55B-LL	293.00	77.70	83.51	370.70	376.51
55B-LH	293.00	80.87	86.92	373.87	379.92
55B-ML	263.61	73.65	79.16	337.26	342.77
55B-MH	263.61	77.78	83.59	341.39	347.20
55B-SL	234.08	69.41	74.60	303.49	308.68
55B-SH	234.08	74.02	79.56	308.10	313.64
55C-LL	328.11	54.83	57.66	382.94	385.77
55C-LH	328.11	57.49	60.46	385.60	388.57

55C-ML	304.17	53.45	56.21	357.62	360.38
55C-MH	304.17	56.18	59.08	360.35	363.25
55C-SL	280.10	51.85	54.52	331.95	334.62
55C-SH	280.10	54.74	57.57	334.84	337.67
56-LL	293.00	65.29	70.24	358.29	363.24
56-LH	293.00	68.75	73.96	361.75	366.96
56-ML	263.61	62.30	67.02	325.91	330.63
56-MH	263.61	66.16	71.17	329.77	334.78
56-SL	234.08	59.42	63.92	293.50	298.00
56-SH	234.08	63.15	67.93	297.23	302.01
58C-LL	687.62	93.47	93.47	781.09	781.09
58C-LH	687.62	107.62	107.62	795.24	795.24
58C-ML	630.43	90.22	90.22	720.65	720.65
58C-MH	630.43	103.25	103.25	733.68	733.68
58C-SL	573.37	86.36	86.36	659.73	659.73
58C-SH	573.37	98.41	98.41	671.78	671.78
58D-LL	687.62	104.05	104.05	791.67	791.67
58D-LH	687.62	117.43	117.43	805.05	805.05
58D-ML	630.43	99.54	99.54	729.97	729.97
58D-MH	630.43	112.88	112.88	743.31	743.31
58D-SL	573.37	96.64	96.64	670.01	670.01
58D-SH	573.37	108.74	108.74	682.11	682.11
60A-LL	687.62	77.68	77.68	765.30	765.3
60A-LH	687.62	87.29	87.29	774.91	774.91
60A-ML	630.43	74.33	74.33	704.76	704.76
60A-MH	630.43	83.96	83.96	714.39	714.39
60A-SL	573.37	72.06	72.06	645.43	645.43
60A-SH	573.37	81.10	81.10	654.47	654.47
61-LL	687.62	79.03	79.03	766.65	766.65
61-LH	687.62	85.96	85.96	773.58	773.58
61-ML	630.43	75.75	75.75	706.18	706.18
61-MH	630.43	83.58	83.58	714.01	714.01
61-SL	573.37	72.59	72.59	645.96	645.96
61-SH	573.37	81.09	81.09	654.46	654.46
62-LL	687.62	80.67	80.67	768.29	768.29
62-LH	687.62	90.21	90.21	777.83	777.83
62-ML	630.43	77.34	77.34	707.77	707.77

62-MH	630.43	87.18	87.18	717.61	717.61
62-SL	573.37	75.18	75.18	648.55	648.55
62-SH	573.37	84.45	84.45	657.82	657.82
63A-LL	328.11	111.27	111.27	439.38	439.38
63A-LH	328.11	126.94	126.94	455.05	455.05
63A-ML	304.17	107.25	107.25	411.42	411.42
63A-MH	304.17	122.50	122.50	426.67	426.67
63A-SL	280.10	103.60	103.60	383.70	383.70
63A-SH	280.10	117.73	117.73	397.83	397.83
63B-LL	328.11	90.41	90.41	418.52	418.52
63B-LH	328.11	98.77	98.77	426.88	426.88
63B-ML	304.17	86.74	86.74	390.91	390.91
63B-MH	304.17	95.59	95.59	399.76	399.76
63B-SL	280.10	83.10	83.10	363.20	363.20
63B-SH	280.10	91.79	91.79	371.89	371.89
64-LL	687.62	70.01	70.01	757.63	757.63
64-LH	687.62	77.75	77.75	765.37	765.37
64-ML	630.43	67.40	67.40	697.83	697.83
64-MH	630.43	75.26	75.26	705.69	705.69
64-SL	573.37	64.91	64.91	638.28	638.28
64-SH	573.37	72.90	72.90	646.27	646.27
65-LL	328.11	99.37	99.62	427.48	427.73
65-LH	328.11	116.59	117.13	444.70	445.24
65-ML	304.17	96.89	97.17	401.06	401.34
65-MH	304.17	113.32	113.91	417.49	418.08
65-SL	280.10	92.57	92.89	372.67	372.99
65-SH	280.10	109.15	109.79	389.25	389.89
66-LL	328.11	97.86	98.04	425.97	426.15
66-LH	328.11	109.87	110.26	437.98	438.37
66-ML	304.17	93.36	93.57	397.53	397.74
66-MH	304.17	106.44	106.88	410.61	411.05
66-SL	280.10	90.50	90.75	370.60	370.85
66-SH	280.10	102.3	102.78	382.40	382.88
67A-LL	687.62	63.52	63.75	751.14	751.37
67A-LH	687.62	72.10	72.60	759.72	760.22
67A-ML	630.43	60.75	61.02	691.18	691.45
67A-MH	630.43	69.38	69.94	699.81	700.37

67A-SL	573.37	58.39	58.72	631.76	632.09
67A-SH	573.37	66.45	67.08	639.82	640.45
70A-LL	1572.34	38.55	42.50	1610.89	1614.84
70A-LH	1572.34	42.34	46.65	1614.68	1618.99
70A-ML	1442.47	37.13	40.92	1479.60	1483.39
70A-MH	1442.47	41.02	45.18	1483.49	1487.65
70A-SL	1312.46	35.64	39.26	1348.10	1351.72
70A-SH	1312.46	39.64	43.62	1352.10	1356.08
70B-LL	1572.34	45.31	53.71	1617.65	1626.05
70B-LH	1572.34	50.43	59.71	1622.77	1632.05
70B-ML	1442.47	43.89	52.00	1486.36	1494.47
70B-MH	1442.47	48.87	57.80	1491.34	1500.27
70B-SL	1312.46	42.30	50.07	1354.76	1362.53
70B-SH	1312.46	47.27	55.82	1359.73	1368.28
71-LL	328.11	65.66	65.83	393.77	393.94
71-LH	328.11	74.73	75.08	402.84	403.19
71-ML	304.17	63.37	63.56	367.54	367.73
71-MH	304.17	72.27	72.66	376.44	376.83
71-SL	280.10	61.26	61.48	341.36	341.58
71-SH	280.10	70.00	70.44	350.10	350.54
72-LL	1572.34	32.76	32.92	1605.10	1605.26
72-LH	1572.34	36.90	37.16	1609.24	1609.50
72-ML	1442.47	31.76	31.95	1474.23	1474.42
72-MH	1442.47	35.80	36.10	1478.27	1478.57
72-SL	1312.46	30.83	31.04	1343.29	1343.50
72-SH	1312.46	34.62	34.97	1347.08	1347.43
73-LL	628.70	34.82	34.86	663.52	663.56
73-LH	628.70	38.35	38.42	667.05	667.12
73-ML	576.96	33.55	33.59	610.51	610.55
73-MH	576.96	37.27	37.34	614.23	614.30
73-SL	530.94	32.48	32.54	563.42	563.48
73-SH	530.94	36.26	36.34	567.20	567.28
74-LL	628.70	57.21	57.30	685.91	686.00
74-LH	628.70	64.94	65.10	693.64	693.80
74-ML	576.96	55.44	55.54	632.40	632.50
74-MH	576.96	62.85	63.03	639.81	639.99
74-SL	530.94	54.01	54.13	584.95	585.07

74-SH	530.94	60.72	60.92	591.66	591.86
75-LL	328.11	61.26	61.36	389.37	389.47
75-LH	328.11	69.08	69.25	397.19	397.36
75-ML	304.17	59.18	59.28	363.35	363.45
75-MH	304.17	67.09	67.29	371.26	371.46
75-SL	280.10	57.47	57.58	337.57	337.68
75-SH	280.10	65.13	65.35	345.23	345.45
76-LL	243.26	67.87	67.96	311.13	311.22
76-LH	243.26	76.19	76.37	319.45	319.63
76-ML	224.04	66.21	66.31	290.25	290.35
76-MH	224.04	73.74	73.93	297.78	297.97
76-SL	204.69	64.66	64.78	269.35	269.47
76-SH	204.69	71.91	72.13	276.60	276.82
77A-LL	1572.34	38.60	44.52	1610.94	1616.86
77A-LH	1572.34	40.62	46.83	1612.96	1619.17
77A-ML	1442.47	36.80	42.43	1479.27	1484.90
77A-MH	1442.47	39.36	45.36	1481.83	1487.83
77A-SL	1312.46	35.00	40.34	1347.46	1352.80
77A-SH	1312.46	38.16	43.96	1350.62	1356.42
77B-LL	1572.34	37.41	42.33	1609.75	1614.67
77B-LH	1572.34	40.63	45.95	1612.97	1618.29
77B-ML	1442.47	35.77	40.45	1478.24	1482.92
77B-MH	1442.47	39.40	44.54	1481.87	1487.01
77B-SL	1312.46	34.38	38.86	1346.84	1351.32
77B-SH	1312.46	38.15	43.09	1350.61	1355.55
77C-LL	1572.34	37.67	41.91	1610.01	1614.25
77C-LH	1572.34	40.98	45.57	1613.32	1617.91
77C-ML	1442.47	36.20	40.26	1478.67	1482.73
77C-MH	1442.47	39.63	44.05	1482.10	1486.52
77C-SL	1312.46	34.65	38.52	1347.11	1350.98
77C-SH	1312.46	38.59	42.88	1351.05	1355.34
77D-LL	1572.34	38.46	47.16	1610.80	1619.50
77D-LH	1572.34	42.07	51.55	1614.41	1623.89
77D-ML	1442.47	37.05	45.42	1479.52	1487.89
77D-MH	1442.47	40.83	50.00	1483.30	1492.47
77D-SL	1312.46	35.50	43.49	1347.96	1355.95
77D-SH	1312.46	39.52	48.33	1351.98	1360.79

77E-LL	1572.34	37.32	41.85	1609.66	1614.19
77E-LH	1572.34	40.09	44.93	1612.43	1617.27
77E-ML	1442.47	35.73	40.05	1478.20	1482.52
77E-MH	1442.47	38.78	43.45	1481.25	1485.92
77E-SL	1312.46	34.07	38.18	1346.53	1350.64
77E-SH	1312.46	37.46	41.94	1349.92	1354.40
78A-LL	1572.34	37.97	46.49	1610.31	1618.83
78A-LH	1572.34	40.35	49.36	1612.69	1621.70
78A-ML	1442.47	36.04	44.10	1478.51	1486.57
78A-MH	1442.47	38.95	47.63	1481.42	1490.10
78A-SL	1312.46	34.41	42.09	1346.87	1354.55
78A-SH	1312.46	37.80	46.19	1350.26	1358.65
78B-LL	1572.34	37.38	42.90	1609.72	1615.24
78B-LH	1572.34	39.48	45.29	1611.82	1617.63
78B-ML	1442.47	35.65	40.91	1478.12	1483.38
78B-MH	1442.47	38.23	43.84	1480.70	1486.31
78B-SL	1312.46	33.95	38.95	1346.41	1351.41
78B-SH	1312.46	36.98	42.37	1349.44	1354.83
78C-LL	1572.34	38.97	44.02	1611.31	1616.36
78C-LH	1572.34	41.58	46.95	1613.92	1619.29
78C-ML	1442.47	37.11	41.90	1479.58	1484.37
78C-MH	1442.47	40.24	45.41	1482.71	1487.88
78C-SL	1312.46	35.36	39.92	1347.82	1352.38
78C-SH	1312.46	38.88	43.86	1351.34	1356.32
79-LL	628.70	44.95	45.32	673.65	674.02
79-LH	628.70	56.89	57.61	685.59	686.31
79-ML	576.96	43.83	44.22	620.79	621.18
79-MH	576.96	55.36	56.10	632.32	633.06
79-SL	530.94	43.87	44.31	574.81	575.25
79-SH	530.94	53.89	54.67	584.83	585.61
80A-LL	628.70	48.54	52.29	677.24	680.99
80A-LH	628.70	50.89	54.81	679.59	683.51
80A-ML	576.96	46.43	50.01	623.39	626.97
80A-MH	576.96	49.31	53.10	626.27	630.06
80A-SL	530.94	44.18	47.58	575.12	578.52
80A-SH	530.94	47.90	51.57	578.84	582.51
80B-LL	628.70	40.81	47.39	669.51	676.09

80B-LH	628.70	42.38	49.19	671.08	677.89
80B-ML	576.96	38.99	45.26	615.95	622.22
80B-MH	576.96	41.16	47.75	618.12	624.71
80B-SL	530.94	37.23	43.21	568.17	574.15
80B-SH	530.94	39.93	46.31	570.87	577.25
81A-LL	1572.34	37.65	43.88	1609.99	1616.22
81A-LH	1572.34	40.15	46.77	1612.49	1619.11
81A-ML	1442.47	36.02	41.96	1478.49	1484.43
81A-MH	1442.47	38.92	45.32	1481.39	1487.79
81A-SL	1312.46	34.39	40.06	1346.85	1352.52
81A-SH	1312.46	37.83	44.02	1350.29	1356.48
81B-LL	1572.34	39.45	41.16	1611.79	1613.50
81B-LH	1572.34	42.43	44.26	1614.77	1616.60
81B-ML	1442.47	37.71	39.34	1480.18	1481.81
81B-MH	1442.47	41.21	42.98	1483.68	1485.45
81B-SL	1312.46	35.92	37.48	1348.38	1349.94
81B-SH	1312.46	39.79	41.50	1352.25	1353.96
81C-LL	1572.34	40.52	40.94	1612.86	1613.28
81C-LH	1572.34	44.79	45.26	1617.13	1617.60
81C-ML	1442.47	38.96	39.37	1481.43	1481.84
81C-MH	1442.47	43.36	43.82	1485.83	1486.29
81C-SL	1312.46	37.21	37.60	1349.67	1350.06
81C-SH	1312.46	41.79	42.23	1354.25	1354.69
81D-LL	1572.34	49.61	54.15	1621.95	1626.49
81D-LH	1572.34	55.19	60.15	1627.53	1632.49
81D-ML	1442.47	48.50	52.93	1490.97	1495.40
81D-MH	1442.47	53.60	58.38	1496.07	1500.85
81D-SL	1312.46	47.20	51.48	1359.66	1363.94
81D-SH	1312.46	51.81	56.39	1364.27	1368.85
82A-LL	1572.34	37.41	42.30	1609.75	1614.64
82A-LH	1572.34	39.40	44.52	1611.74	1616.86
82A-ML	1442.47	35.58	40.22	1478.05	1482.69
82A-MH	1442.47	38.09	43.04	1480.56	1485.51
82A-SL	1312.46	33.79	38.19	1346.25	1350.65
82A-SH	1312.46	36.98	41.77	1349.44	1354.23
82B-LL	628.43	52.24	58.12	680.67	686.55
82B-LH	628.43	54.32	60.42	682.75	688.85

82B-ML	576.96	50.00	55.62	626.96	632.58
82B-MH	576.96	52.76	58.68	629.72	635.64
82B-SL	530.81	47.64	52.98	578.45	583.79
82B-SH	530.81	51.18	56.89	581.99	587.70
83A-LL	628.70	40.01	43.49	668.71	672.19
83A-LH	628.70	42.39	46.07	671.09	674.77
83A-ML	576.96	38.36	41.70	615.32	618.66
83A-MH	576.96	41.06	44.62	618.02	621.58
83A-SL	530.94	36.78	39.98	567.72	570.92
83A-SH	530.94	40.00	43.46	570.94	574.40
83B-LL	628.70	40.79	46.32	669.49	675.02
83B-LH	628.70	40.85	46.37	669.55	675.07
83B-ML	576.96	38.78	44.03	615.74	620.99
83B-MH	576.96	39.48	44.81	616.44	621.77
83B-SL	530.94	36.70	41.67	567.64	572.61
83B-SH	530.94	38.32	43.49	569.26	574.43
83C-LL	628.70	43.17	43.21	671.87	671.91
83C-LH	628.70	42.78	42.81	671.48	671.51
83C-ML	576.96	40.95	40.99	617.91	617.95
83C-MH	576.96	41.34	41.38	618.30	618.34
83C-SL	530.94	38.65	38.69	569.59	569.63
83C-SH	530.94	40.00	40.04	570.94	570.98
83D-LL	628.70	41.51	42.99	670.21	671.69
83D-LH	628.70	40.64	42.09	669.34	670.79
83D-ML	576.96	39.39	40.79	616.35	617.75
83D-MH	576.96	38.84	40.22	615.80	617.18
83D-SL	530.94	37.10	38.42	568.04	569.36
83D-SH	530.94	37.37	38.70	568.31	569.64
83E-LL	628.70	42.19	46.61	670.89	675.31
83E-LH	628.70	42.04	46.43	670.74	675.13
83E-ML	576.96	40.19	44.39	617.15	621.35
83E-MH	576.96	40.46	44.68	617.42	621.64
83E-SL	530.94	37.89	41.85	568.83	572.79
83E-SH	530.94	39.31	43.40	570.25	574.34
84A-LL	628.70	50.68	55.87	679.38	684.57
84A-LH	628.70	55.69	61.37	684.39	690.07
84A-ML	576.96	48.81	53.79	625.77	630.75

84A-MH	576.96	53.93	59.42	630.89	636.38
84A-SL	530.94	46.92	51.70	577.86	582.64
84A-SH	530.94	52.09	57.35	583.03	588.29
84B-LL	628.70	44.68	49.34	673.38	678.04
84B-LH	628.70	50.47	55.61	679.17	684.31
84B-ML	576.96	43.59	48.11	620.55	625.07
84B-MH	576.96	49.04	53.99	626.00	630.95
84B-SL	530.94	42.36	46.71	573.30	577.65
84B-SH	530.94	47.37	52.10	578.31	583.04
84C-LL	628.70	41.95	43.84	670.65	672.54
84C-LH	628.70	45.16	47.19	673.86	675.89
84C-ML	576.96	40.44	42.26	617.40	619.22
84C-MH	576.96	43.90	45.87	620.86	622.83
84C-SL	530.94	38.70	40.44	569.64	571.38
84C-SH	530.94	42.54	44.44	573.48	575.38
85-LL	628.70	43.65	45.18	672.35	673.88
85-LH	628.70	48.73	50.43	677.43	679.13
85-ML	576.96	42.17	43.65	619.13	620.61
85-MH	576.96	47.23	48.87	624.19	625.83
85-SL	530.94	40.87	42.29	571.81	573.23
85-SH	530.94	45.46	47.02	576.40	577.96
86A-LL	628.70	41.24	42.25	669.94	670.95
86A-LH	628.70	45.14	46.25	673.84	674.95
86A-ML	576.96	39.62	40.59	616.58	617.55
86A-MH	576.96	43.88	44.95	620.84	621.91
86A-SL	530.94	38.05	38.98	568.99	569.92
86A-SH	530.94	42.35	43.38	573.29	574.32
86B-LL	628.70	45.68	46.80	674.38	675.50
86B-LH	628.70	51.36	52.61	680.06	681.31
86B-ML	576.96	44.48	45.56	621.44	622.52
86B-MH	576.96	50.07	51.29	627.03	628.25
86B-SL	530.94	43.15	44.19	574.09	575.13
86B-SH	530.94	48.64	49.83	579.58	580.77
87A-LL	628.70	43.94	45.76	672.64	674.46
87A-LH	628.70	50.17	52.25	678.87	680.95
87A-ML	576.96	42.51	44.27	619.47	621.23
87A-MH	576.96	48.81	50.83	625.77	627.79

87A-SL	530.94	41.76	43.49	572.70	574.43
87A-SH	530.94	47.33	49.29	578.27	580.23
87B-LL	243.26	50.02	52.96	293.28	296.22
87B-LH	243.26	61.53	65.15	304.79	308.41
87B-ML	224.04	49.42	52.32	273.46	276.36
87B-MH	224.04	60.78	64.34	284.82	288.38
87B-SL	204.69	48.90	51.77	253.59	256.46
87B-SH	204.69	58.75	62.20	263.44	266.89

LL- large body weight, low lactation, LH- large body weight, high lactation, ML- moderate body weight, low lactation, MH- moderate body weight, high lactation, SL- small body weight, low lactation, SH- small body weight, high lactation

Table A.2

Irrigation estimates for diets formulated with corn and sorghum for a 100-head cow-calf herd with various genetic potential for mature weight and peak lactation in the Great Plains (Megaliters)

MLRA	Irrigation for corn diets	Irrigation for sorghum diets
102A-LL	15.88	35.88
102A-LH	16.67	37.65
102A-ML	15.22	34.38
102A-MH	16.00	36.14
102A-SL	14.49	32.73
102A-SH	15.38	34.74
102B-LL	13.31	80.45
102B-LH	13.93	84.21
102B-ML	12.76	77.13
102B-MH	13.47	81.46
102B-SL	12.24	73.99
102B-SH	12.91	78.06
102C-LL	13.43	24.79
102C-LH	14.04	25.92
102C-ML	12.76	23.56
102C-MH	13.48	24.89
102C-SL	12.11	22.35
102C-SH	12.91	23.83
106-LL	14.33	18.6
106-LH	15.2	19.72
106-ML	13.91	18.06
106-MH	14.84	19.26
106-SL	13.44	17.44
106-SH	14.37	18.65

112-LL	14.18	19.31
112-LH	14.78	20.13
112-ML	13.90	18.93
112-MH	14.51	19.77
112-SL	13.56	18.47
112-SH	14.21	19.36
116A-LL	14.96	29.99
116A-LH	15.65	31.37
116A-ML	14.52	29.11
116A-MH	15.31	30.69
116A-SL	13.97	28.00
116A-SH	14.91	29.89
116B-LL	15.52	24.80
116B-LH	16.16	25.83
116B-ML	14.99	23.96
116B-MH	15.75	25.17
116B-SL	14.38	22.97
116B-SH	15.31	24.47
117-LL	15.43	53.89
117-LH	16.26	56.79
117-ML	14.93	52.17
117-MH	15.86	55.4
117-SL	14.39	50.26
117-SH	15.47	54.05
118A-LL	18.33	34.24
118A-LH	20.41	38.14
118A-ML	17.68	33.02
118A-MH	19.72	36.84
118A-SL	17.03	31.82

118A-SH	19.13	35.74
118B-LL	17.49	32.85
118B-LH	18.47	34.69
118B-ML	16.89	31.73
118B-MH	17.93	33.69
118B-SL	16.24	30.51
118B-SH	17.49	32.85
119-LL	15.64	33.16
119-LH	19.33	40.97
119-ML	15.40	32.65
119-MH	18.90	40.08
119-SL	15.39	32.64
119-SH	18.27	38.72
133B-LL	12.28	22.63
133B-LH	14.92	27.49
133B-ML	11.87	21.88
133B-MH	14.35	26.45
133B-SL	11.99	22.10
133B-SH	13.72	25.29
135B-LL	14.05	34.68
135B-LH	17.59	43.41
135B-ML	13.88	34.26
135B-MH	17.23	42.51
135B-SL	13.65	33.68
135B-SH	16.45	40.59
150A-LL	9.51	15.03
150A-LH	9.88	15.61
150A-ML	8.99	14.21
150A-MH	9.61	15.18

150A-SL	8.61	13.6
150A-SH	9.36	14.78
150B-LL	14.84	20.45
150B-LH	16.35	22.53
150B-ML	14.43	19.88
150B-MH	16.03	22.09
150B-SL	14.02	19.32
150B-SH	15.64	21.56
152B-LL	20.07	18.45
152B-LH	24.52	22.54
152B-ML	19.81	18.21
152B-MH	23.86	21.94
152B-SL	19.57	17.99
152B-SH	22.96	21.11
42-LL	13.04	30.09
42-LH	14.52	33.50
42-ML	12.77	29.46
42-MH	13.93	32.14
42-SL	12.25	28.26
42-SH	13.33	30.77
53A-LL	66.92	66.92
53A-LH	64.94	64.94
53A-ML	63.01	63.01
53A-MH	61.13	61.13
53A-SL	58.81	58.81
53A-SH	57.84	57.84
53B-LL	85.36	85.36
53B-LH	92.77	92.77
53B-ML	81.68	81.68

53B-MH	89.49	89.49
53B-SL	78.24	78.24
53B-SH	85.63	85.63
53C-LL	91.05	91.05
53C-LH	99.81	99.81
53C-ML	87.62	87.62
53C-MH	96.73	96.73
53C-SL	83.74	83.74
53C-SH	93.19	93.19
54-LL	69.01	69.01
54-LH	75.47	75.47
54-ML	65.85	65.85
54-MH	73.38	73.38
54-SL	64.03	64.03
54-SH	70.91	70.91
55A-LL	19.97	29.74
55A-LH	21.01	31.29
55A-ML	19.33	28.80
55A-MH	20.41	30.40
55A-SL	18.72	27.89
55A-SH	19.85	29.57
55B-LL	19.35	39.60
55B-LH	20.14	41.22
55B-ML	18.34	37.54
55B-MH	19.37	39.64
55B-SL	17.28	35.38
55B-SH	18.43	37.73
55C-LL	18.07	27.25
55C-LH	18.94	28.58

55C-ML	17.61	26.57
55C-MH	18.51	27.93
55C-SL	17.08	25.77
55C-SH	18.04	27.21
56-LL	16.45	34.02
56-LH	17.32	35.83
56-ML	15.69	32.46
56-MH	16.67	34.48
56-SL	14.97	30.96
56-SH	15.91	32.91
58C-LL	96.88	96.88
58C-LH	111.55	111.55
58C-ML	93.51	93.51
58C-MH	107.02	107.02
58C-SL	89.51	89.51
58C-SH	102.00	102.00
58D-LL	123.26	123.26
58D-LH	139.11	139.11
58D-ML	117.91	117.91
58D-MH	133.72	133.72
58D-SL	114.49	114.49
58D-SH	128.81	128.81
60A-LL	18.06	18.06
60A-LH	20.29	20.29
60A-ML	17.28	17.28
60A-MH	19.51	19.51
60A-SL	16.75	16.75
60A-SH	18.85	18.85
61-LL	76.43	76.43

61-LH	83.13	83.13
61-ML	73.25	73.25
61-MH	80.83	80.83
61-SL	70.20	70.20
61-SH	78.42	78.42
62-LL	63.75	63.75
62-LH	71.29	71.29
62-ML	61.12	61.12
62-MH	68.9	68.9
62-SL	59.42	59.42
62-SH	66.74	66.74
63A-LL	138.25	138.25
63A-LH	157.71	157.71
63A-ML	133.25	133.25
63A-MH	152.20	152.20
63A-SL	128.72	128.72
63A-SH	146.27	146.27
63B-LL	83.59	83.59
63B-LH	91.31	91.31
63B-ML	80.19	80.19
63B-MH	88.37	88.37
63B-SL	76.83	76.83
63B-SH	84.86	84.86
64-LL	36.90	36.90
64-LH	40.98	40.98
64-ML	35.53	35.53
64-MH	39.67	39.67
64-SL	34.22	34.22
64-SH	38.43	38.43

65-LL	65.67	66.62
65-LH	72.91	74.93
65-ML	63.39	64.45
65-MH	69.74	71.95
65-SL	59.72	60.92
65-SH	65.91	68.31
66-LL	77.66	78.36
66-LH	83.29	84.76
66-ML	73.46	74.23
66-MH	79.53	81.15
66-SL	70.31	71.22
66-SH	75.19	76.97
67A-LL	30.55	31.52
67A-LH	33.37	35.44
67A-ML	28.94	30.08
67A-MH	31.67	33.99
67A-SL	27.46	28.82
67A-SH	29.80	32.42
70A-LL	6.21	22.54
70A-LH	6.78	24.64
70A-ML	5.96	21.63
70A-MH	6.54	23.74
70A-SL	5.70	20.70
70A-SH	6.26	22.73
70B-LL	9.42	47.35
70B-LH	10.4	52.29
70B-ML	9.08	45.68
70B-MH	10.01	50.35
70B-SL	8.72	43.84

70B-SH	9.59	48.21
71-LL	30.97	31.54
71-LH	33.97	35.15
71-ML	29.66	30.31
71-MH	32.40	33.73
71-SL	28.36	29.12
71-SH	30.89	32.38
72-LL	27.87	28.43
72-LH	30.27	31.20
72-ML	26.63	27.27
72-MH	28.81	29.87
72-SL	25.40	26.15
72-SH	27.17	28.38
73-LL	39.81	39.87
73-LH	42.76	42.86
73-ML	37.96	38.03
73-MH	41.05	41.17
73-SL	36.31	36.39
73-SH	39.25	39.38
74-LL	37.13	37.38
74-LH	40.47	40.92
74-ML	35.56	35.84
74-MH	38.43	38.93
74-SL	34.09	34.42
74-SH	36.30	36.87
75-LL	28.59	28.90
75-LH	31.27	31.82
75-ML	27.44	27.78
75-MH	29.95	30.58

75-SL	26.41	26.78
75-SH	28.60	29.32
76-LL	42.96	43.18
76-LH	46.10	46.53
76-ML	41.47	41.73
76-MH	43.83	44.31
76-SL	39.79	40.09
76-SH	41.87	42.42
77A-LL	9.61	35.32
77A-LH	10.08	37.03
77A-ML	9.14	33.58
77A-MH	9.74	35.8
77A-SL	8.67	31.86
77A-SH	9.41	34.55
77B-LL	5.88	24.97
77B-LH	6.37	27.01
77B-ML	5.61	23.80
77B-MH	6.15	26.08
77B-SL	5.37	22.80
77B-SH	5.91	25.07
77C-LL	8.10	24.95
77C-LH	8.77	27.04
77C-ML	7.76	23.90
77C-MH	8.46	26.07
77C-SL	7.40	22.82
77C-SH	8.18	25.22
77D-LL	11.32	54.43
77D-LH	12.33	59.27
77D-ML	10.87	52.27

77D-MH	11.92	57.3
77D-SL	10.39	49.94
77D-SH	11.45	55.05
77E-LL	5.35	22.49
77E-LH	5.73	24.06
77E-ML	5.11	21.47
77E-MH	5.52	23.20
77E-SL	4.86	20.42
77E-SH	5.30	22.29
78A-LL	10.28	43.84
78A-LH	10.88	46.42
78A-ML	9.73	41.52
78A-MH	10.48	44.70
78A-SL	9.27	39.55
78A-SH	10.13	43.22
78B-LL	7.68	28.17
78B-LH	8.07	29.62
78B-ML	7.31	26.82
78B-MH	7.79	28.60
78B-SL	6.94	25.47
78B-SH	7.50	27.52
78C-LL	14.31	32.25
78C-LH	15.21	34.27
78C-ML	13.59	30.63
78C-MH	14.68	33.08
78C-SL	12.93	29.13
78C-SH	14.12	31.81
79-LL	35.89	37.12
79-LH	40.92	43.32

79-ML	34.37	35.68
79-MH	38.99	41.47
79-SL	33.56	35.03
79-SH	37.16	39.73
80A-LL	14.13	28.34
80A-LH	14.76	29.60
80A-ML	13.49	27.05
80A-MH	14.27	28.61
80A-SL	12.80	25.66
80A-SH	13.81	27.70
80B-LL	14.33	40.02
80B-LH	14.83	41.43
80B-ML	13.66	38.16
80B-MH	14.37	40.15
80B-SL	13.02	36.35
80B-SH	13.91	38.86
81A-LL	10.62	39.02
81A-LH	11.28	41.46
81A-ML	10.13	37.25
81A-MH	10.91	40.08
81A-SL	9.66	35.49
81A-SH	10.55	38.78
81B-LL	19.77	26.70
81B-LH	21.18	28.61
81B-ML	18.85	25.46
81B-MH	20.52	27.72
81B-SL	17.92	24.21
81B-SH	19.73	26.65
81C-LL	18.77	22.47

81C-LH	20.67	24.74
81C-ML	18.00	21.54
81C-MH	19.95	23.88
81C-SL	17.16	20.54
81C-SH	19.11	22.88
81D-LL	12.40	37.41
81D-LH	13.54	40.84
81D-ML	12.08	36.44
81D-MH	13.04	39.35
81D-SL	11.69	35.28
81D-SH	12.51	37.73
82A-LL	10.22	30.67
82A-LH	10.72	32.16
82A-ML	9.70	29.11
82A-MH	10.34	31.03
82A-SL	9.20	27.59
82A-SH	10.01	30.02
82B-LL	18.75	43.91
82B-LH	19.42	45.49
82B-ML	17.91	41.93
82B-MH	18.83	44.10
82B-SL	17.02	39.86
82B-SH	18.20	42.63
83A-LL	17.59	32.50
83A-LH	18.58	34.33
83A-ML	16.84	31.12
83A-MH	17.96	33.18
83A-SL	16.11	29.77
83A-SH	17.47	32.27

83B-LL	18.09	49.96
83B-LH	18.07	49.91
83B-ML	17.18	47.46
83B-MH	17.44	48.17
83B-SL	16.24	44.87
83B-SH	16.90	46.70
83C-LL	26.58	30.22
83C-LH	26.28	29.88
83C-ML	25.19	28.65
83C-MH	25.36	28.84
83C-SL	23.75	27.01
83C-SH	24.51	27.87
83D-LL	22.48	32.17
83D-LH	21.97	31.45
83D-ML	21.32	30.52
83D-MH	20.98	30.03
83D-SL	20.07	28.73
83D-SH	20.17	28.87
83E-LL	22.43	47.79
83E-LH	22.30	47.51
83E-ML	21.35	45.49
83E-MH	21.44	45.68
83E-SL	20.11	42.84
83E-SH	20.80	44.33
84A-LL	11.75	29.79
84A-LH	12.86	32.60
84A-ML	11.29	28.61
84A-MH	12.41	31.46
84A-SL	10.82	27.43

84A-SH	11.91	30.19
84B-LL	18.57	39.30
84B-LH	20.49	43.36
84B-ML	18.01	38.11
84B-MH	19.72	41.74
84B-SL	17.36	36.74
84B-SH	18.87	39.93
84C-LL	18.09	25.13
84C-LH	19.41	26.96
84C-ML	17.40	24.16
84C-MH	18.83	26.15
84C-SL	16.62	23.08
84C-SH	18.19	25.26
85-LL	14.36	21.45
85-LH	15.91	23.77
85-ML	13.83	20.66
85-MH	15.34	22.92
85-SL	13.36	19.96
85-SH	14.63	21.85
86A-LL	14.84	19.36
86A-LH	16.18	21.11
86A-ML	14.22	18.55
86A-MH	15.69	20.46
86A-SL	13.62	17.77
86A-SH	15.07	19.66
86B-LL	20.62	24.63
86B-LH	23.18	27.69
86B-ML	20.08	23.98
86B-MH	22.60	27.00

86B-SL	19.48	23.26
86B-SH	21.96	26.23
87A-LL	12.21	20.32
87A-LH	13.94	23.20
87A-ML	11.81	19.66
87A-MH	13.56	22.57
87A-SL	11.60	19.31
87A-SH	13.15	21.88
87B-LL	11.91	19.42
87B-LH	14.65	23.89
87B-ML	11.77	19.18
87B-MH	14.47	23.59
87B-SL	11.64	18.98
87B-SH	13.99	22.81

LL- large body weight, low lactation, LH- large body weight, high lactation, ML- moderate body weight, low lactation, MH- moderate body weight, high lactation, SL- small body weight, low lactation, SH- small body weight, high lactation

Table A.4

Estimates of fertilizer application rates for corn and sorghum-based diets for a 100-head cow-calf herd with various genetic potentials for mature weight and peak lactation in the Great Plains (kilograms per year)

	Corn-based diets			**Sorghum-based diets**		
MLRA	*Nitrogen*	*Phosphorus*	*Potassium*	*Nitrogen*	*Phosphorus*	*Potassium*
102A-LL	18321	37079	65830	18345	37138	65630
102A-LH	18498	37470	66521	18524	37532	66311
102A-ML	16693	33823	60045	16717	33880	59853
102A-MH	16870	34213	60733	16895	34272	60531
102A-SL	15045	30522	54180	15067	30575	53997
102A-SH	15247	30967	54966	15270	31024	54771
102B-LL	19342	35320	62708	19365	35376	62519
102B-LH	19501	35608	63216	19525	35667	63019
102B-ML	17602	32141	57060	17624	32195	56879
102B-MH	17785	32474	57646	17808	32530	57455
102B-SL	15863	28963	51414	15884	29014	51240
102B-SH	16034	29276	51965	16056	29330	51781
102C-LL	17634	35595	63187	17659	35656	62978
102C-LH	17804	35888	63704	17831	35952	63486
102C-ML	16055	32351	57424	16079	32409	57226
102C-MH	16256	32696	58033	16281	32757	57823
102C-SL	14473	29099	51649	14496	29155	51461
102C-SH	14697	29484	52327	14721	29543	52126
106-LL	16817	31265	55502	16839	31318	55321
106-LH	17014	31693	56259	17037	31750	56068
106-ML	15651	29149	51744	15672	29201	51569
106-MH	15860	29605	52549	15883	29660	52362
106-SL	14463	26989	47906	14483	27039	47736
106-SH	14674	27448	48717	14695	27501	48536
112-LL	17278	30195	53608	17297	30244	53443
112-LH	17402	30448	54054	17423	30499	53882
112-ML	16088	28166	50002	16108	28214	49840
112-MH	16216	28425	50458	16236	28474	50290

112-SL	14877	26096	46324	14897	26143	46166
112-SH	15014	26374	46813	15034	26422	46648
116A-LL	18045	30402	53957	18019	30401	53672
116A-LH	18217	30688	54462	18190	30688	54164
116A-ML	16804	28308	50237	16779	28307	49960
116A-MH	17001	28635	50814	16975	28635	50522
116A-SL	15528	26154	46412	15504	26154	46146
116A-SH	15762	26544	47099	15736	26543	46815
116B-LL	18095	31031	55074	18068	31030	54785
116B-LH	18251	31313	55571	18223	31312	55271
116B-ML	16835	28886	51264	16809	28886	50985
116B-MH	17020	29221	51855	16993	29220	51562
116B-SL	15546	26690	47364	15522	26690	47096
116B-SH	15773	27101	48090	15747	27101	47805
117-LL	18025	31903	56626	17999	31903	56343
117-LH	18225	32317	57358	18197	32317	57060
117-ML	16776	29745	52793	16751	29745	52519
117-MH	16997	30206	53607	16971	30206	53316
117-SL	15505	27547	48889	15481	27547	48625
117-SH	15765	28089	49845	15740	28088	49561
118A-LL	17915	31296	55550	17890	31295	55275
118A-LH	18324	32104	56976	18296	32103	56670
118A-ML	16656	29132	51707	16632	29132	51441
118A-MH	17057	29923	53103	17030	29923	52807
118A-SL	15391	26958	47844	15367	26957	47588
118A-SH	15802	27771	49279	15776	27770	48992
118B-LL	18453	30574	54275	18431	30574	54027
118B-LH	18639	30950	54938	18615	30949	54676
118B-ML	17140	28450	50501	17118	28450	50261
118B-MH	17338	28852	51211	17315	28851	50957
118B-SL	15810	26296	46676	15789	26296	46445
118B-SH	16047	26777	47524	16025	26776	47276
119-LL	18469	30528	54196	18447	30528	53955
119-LH	19211	32019	56829	19184	32019	56531

119-ML	17209	28518	50623	17188	28518	50386
119-MH	17916	29936	53128	17889	29936	52836
119-SL	15990	26592	47199	15969	26591	46961
119-SH	16569	27754	49250	16543	27753	48969
133B-LL	14935	30387	53932	14909	30387	53649
133B-LH	15730	31717	56277	15698	31717	55933
133B-ML	13925	28271	50172	13900	28270	49899
133B-MH	14671	29519	52374	14641	29519	52043
133B-SL	13067	26406	46856	13042	26405	46579
133B-SH	13588	27278	48395	13560	27278	48078
135B-LL	17350	29803	52905	17328	29803	52659
135B-LH	18160	31214	55394	18132	31214	55086
135B-ML	16195	27824	49388	16173	27824	49145
135B-MH	16960	29158	51740	16933	29157	51439
135B-SL	15016	25805	45799	14994	25804	45560
135B-SH	15658	26923	47771	15632	26922	47483
150A-LL	26512	29010	51504	26492	29010	51284
150A-LH	26623	29195	51830	26602	29195	51602
150A-ML	24487	26835	47640	24468	26834	47432
150A-MH	24672	27145	48187	24652	27145	47965
150A-SL	22491	24717	43878	22473	24716	43679
150A-SH	22717	25094	44543	22697	25094	44327
150B-LL	21143	29293	52003	21122	29293	51771
150B-LH	21452	29811	52915	21429	29810	52659
150B-ML	19629	27240	48354	19608	27240	48128
150B-MH	19957	27790	49325	19934	27790	49073
150B-SL	18106	25176	44687	18086	25175	44467
150B-SH	18438	25733	45670	18416	25733	45425
152B-LL	16575	29879	53036	16552	29879	52777
152B-LH	17326	31137	55254	17297	31137	54937
152B-ML	15490	27893	49507	15466	27893	49251
152B-MH	16174	29040	51528	16146	29039	51220
152B-SL	14400	25899	45963	14377	25899	45710
152B-SH	14973	26859	47655	14945	26859	47359

42-LL	28739	160544	285346	28720	160543	285142
42-LH	29121	161135	286391	29101	161135	286164
42-ML	26550	147568	262280	26532	147568	262080
42-MH	26870	148064	263156	26850	148064	262938
42-SL	24309	134501	239052	24291	134501	238861
42-SH	24615	134977	239894	24596	134977	239685
53A-LL	27307	1830220	5400426	27307	1830220	5400426
53A-LH	27248	1778208	5244588	27248	1778208	5244588
53A-ML	25086	1721574	5081829	25086	1721574	5081829
53A-MH	25030	1672133	4933693	25030	1672133	4933693
53A-SL	22861	1605467	4740863	22861	1605467	4740863
53A-SH	22831	1579751	4663810	22831	1579751	4663810
53B-LL	13229	2521534	7514865	13229	2521534	7514865
53B-LH	13456	2737500	8161907	13456	2737500	8161907
53B-ML	12342	2411917	7189348	12342	2411917	7189348
53B-MH	12582	2639728	7871879	12582	2639728	7871879
53B-SL	11458	2309227	6884601	11458	2309227	6884601
53B-SH	11685	2524755	7530334	11685	2524755	7530334
53C-LL	15941	2282433	6797837	15941	2282433	6797837
53C-LH	16238	2498800	7446018	16238	2498800	7446018
53C-ML	14887	2195178	6539344	14887	2195178	6539344
53C-MH	15195	2420175	7213379	15195	2420175	7213379
53C-SL	13812	2096987	6248104	13812	2096987	6248104
53C-SH	14132	2330359	6947229	14132	2330359	6947229
54-LL	19671	1890903	5582028	19671	1890903	5582028
54-LH	19815	2061670	6093668	19815	2061670	6093668
54-ML	18093	1801888	5322260	18093	1801888	5322260
54-MH	18260	2000754	5918087	18260	2000754	5918087
54-SL	16547	1748025	5167795	16547	1748025	5167795
54-SH	16700	1929733	5712214	16700	1929733	5712214
55A-LL	18767	40329	71609	18791	40387	71412
55A-LH	18951	40730	72318	18977	40791	72110
55A-ML	17544	37704	66945	17567	37760	66754
55A-MH	17734	38118	67676	17758	38177	67475

55A-SL	16318	35074	62273	16341	35129	62088
55A-SH	16518	35508	63038	16541	35565	62842
55B-LL	16072	37285	66186	16099	37350	65964
55B-LH	16235	37617	66773	16263	37685	66542
55B-ML	14652	33937	60240	14678	33999	60030
55B-MH	14864	34369	61003	14891	34435	60781
55B-SL	13217	30556	54234	13241	30614	54036
55B-SH	13453	31039	55087	13479	31101	54875
55C-LL	18113	38410	68202	18136	38465	68015
55C-LH	18277	38691	68698	18300	38749	68501
55C-ML	16953	35884	63714	16975	35938	63531
55C-MH	17120	36172	64221	17143	36228	64029
55C-SL	15772	33321	59159	15794	33373	58982
55C-SH	15950	33626	59697	15972	33681	59510
56-LL	19715	36013	63936	19738	36071	63738
56-LH	19902	36377	64578	19927	36438	64370
56-ML	17930	32775	58183	17953	32830	57994
56-MH	18140	33181	58900	18164	33240	58700
56-SL	16144	29534	52425	16165	29587	52246
56-SH	16346	29926	53117	16369	29982	52926
58C-LL	13129	2238798	6623412	13129	2238798	6623412
58C-LH	13329	2567467	7607997	13329	2567467	7607997
58C-ML	12101	2157802	6387701	12101	2157802	6387701
58C-MH	12285	2460279	7293823	12285	2460279	7293823
58C-SL	11067	2062439	6108936	11067	2062439	6108936
58C-SH	11237	2342202	6947017	11237	2342202	6947017
58D-LL	17152	2038571	6021728	17152	2038571	6021728
58D-LH	17395	2291877	6780310	17395	2291877	6780310
58D-ML	15801	1947420	5755678	15801	1947420	5755678
58D-MH	16044	2200128	6512471	16044	2200128	6512471
58D-SL	14482	1886956	5581512	14482	1886956	5581512
58D-SH	14702	2115949	6267284	14702	2115949	6267284
60A-LL	16890	2031881	6003691	16890	2031881	6003691
60A-LH	17079	2274784	6731367	17079	2274784	6731367

60A-ML	15546	1941455	5739728	15546	1941455	5739728
60A-MH	15737	2184928	6469111	15737	2184928	6469111
60A-SL	14227	1878439	5557861	14227	1878439	5557861
60A-SH	14406	2106996	6242558	14406	2106996	6242558
61-LL	22925	1754313	5171099	22925	1754313	5171099
61-LH	23105	1902281	5614280	23105	1902281	5614280
61-ML	21104	1678641	4951378	21104	1678641	4951378
61-MH	21308	1845749	5451887	21308	1845749	5451887
61-SL	19290	1605570	4739432	19290	1605570	4739432
61-SH	19511	1786860	5282417	19511	1786860	5282417
62-LL	21425	1792289	5284854	21425	1792289	5284854
62-LH	21657	1996194	5895574	21657	1996194	5895574
62-ML	19726	1715571	5061998	19726	1715571	5061998
62-MH	19964	1925879	5691896	19964	1925879	5691896
62-SL	18058	1663751	4913701	18058	1663751	4913701
62-SH	18283	1861681	5506526	18283	1861681	5506526
63A-LL	12485	2392915	7127738	12485	2392915	7127738
63A-LH	12868	2725154	8122891	12868	2725154	8122891
63A-ML	11675	2305153	6867764	11675	2305153	6867764
63A-MH	12048	2628693	7836860	12048	2628693	7836860
63A-SL	10869	2225484	6632047	10869	2225484	6632047
63A-SH	11215	2525161	7529666	11215	2525161	7529666
63B-LL	13691	2399194	7148201	13691	2399194	7148201
63B-LH	13934	2617847	7803284	13934	2617847	7803284
63B-ML	12777	2300560	6855597	12777	2300560	6855597
63B-MH	13034	2532302	7549894	13034	2532302	7549894
63B-SL	11860	2202986	6566182	11860	2202986	6566182
63B-SH	12112	2430415	7247558	12112	2430415	7247558
64-LL	19784	1869732	5517691	19784	1869732	5517691
64-LH	19973	2068852	6114178	19973	2068852	6114178
64-ML	18217	1796893	5306421	18217	1796893	5306421
64-MH	18409	1999076	5912082	18409	1999076	5912082
64-SL	16657	1727297	5104853	16657	1727297	5104853
64-SH	16852	1932749	5720307	16852	1932749	5720307

65-LL	14674	2048119	6093429	14673	2048119	6093417
65-LH	15272	2253226	6706731	15270	2253226	6706706
65-ML	13763	1973060	5871422	13762	1973060	5871409
65-MH	14341	2149281	6398145	14339	2149281	6398118
65-SL	12791	1854649	5519575	12790	1854649	5519560
65-SH	13376	2024913	6028402	13374	2024913	6028372
66-LL	14380	2170730	6461774	14379	2170730	6461764
66-LH	14793	2309873	6877808	14791	2309873	6877786
66-ML	13419	2050054	6103124	13418	2050054	6103113
66-MH	13870	2199552	6550096	13867	2199552	6550072
66-SL	12507	1957547	5828812	12506	1957547	5828799
66-SH	12920	2073617	6175637	12917	2073617	6175611
67A-LL	13322	2095832	6196749	13321	2095832	6196739
67A-LH	13493	2242129	6634614	13491	2242129	6634594
67A-ML	12262	1974379	5839643	12261	1974379	5839632
67A-MH	12436	2111763	6250760	12434	2111763	6250736
67A-SL	11212	1859502	5502198	11211	1859502	5502184
67A-SH	11380	1967579	5825453	11377	1967579	5825427
70A-LL	25574	160618	285481	25557	160617	285286
70A-LH	25675	161029	286207	25656	161029	285994
70A-ML	23508	147542	262238	23491	147542	262052
70A-MH	23611	147964	262983	23593	147964	262779
70A-SL	21439	134446	238958	21422	134445	238779
70A-SH	21542	134877	239720	21524	134877	239524
70B-LL	29372	161193	286503	29355	161192	286309
70B-LH	29509	161732	287455	29489	161731	287240
70B-ML	27008	148124	263271	26991	148123	263084
70B-MH	27140	148646	264194	27121	148646	263988
70B-SL	24637	135021	239980	24621	135021	239801
70B-SH	24766	135542	240900	24748	135542	240702
71-LL	16396	1980502	5894358	16395	1980502	5894349
71-LH	16776	2145281	6387635	16774	2145281	6387617
71-ML	15302	1891900	5631706	15301	1891900	5631696
71-MH	15679	2035908	6062677	15677	2035908	6062657

71-SL	14210	1801674	5364175	14209	1801674	5364163
71-SH	14585	1930269	5748917	14583	1930269	5748894
72-LL	39834	1476545	4234826	39833	1476545	4234816
72-LH	39945	1573090	4523972	39944	1573090	4523955
72-ML	36589	1398933	4017882	36588	1398933	4017871
72-MH	36700	1483544	4271232	36698	1483544	4271213
72-SL	33342	1321495	3801466	33341	1321495	3801453
72-SH	33450	1383215	3986163	33448	1383215	3986142
73-LL	26035	1449297	4267751	26034	1449297	4267743
73-LH	26170	1537701	4532563	26169	1537701	4532550
73-ML	23952	1374538	4049890	23951	1374538	4049881
73-MH	24096	1466593	4325633	24094	1466593	4325618
73-SL	22103	1306598	3851770	22102	1306598	3851760
73-SH	22251	1390523	4103112	22250	1390523	4103095
74-LL	38966	1440728	4239299	38965	1440728	4239289
74-LH	39400	1547000	4557206	39398	1547000	4557189
74-ML	35921	1372686	4041654	35920	1372686	4041643
74-MH	36341	1458999	4299711	36339	1458999	4299692
74-SL	33223	1308053	3853498	33222	1308053	3853485
74-SH	33608	1367703	4031643	33606	1367703	4031622
75-LL	19091	1837621	5466141	19090	1837621	5466132
75-LH	19471	1989922	5922128	19469	1989922	5922112
75-ML	17811	1759695	5235496	17810	1759695	5235487
75-MH	18201	1897489	5647945	18199	1897489	5647927
75-SL	16543	1687895	5023205	16542	1687895	5023194
75-SH	16926	1803143	5368033	16924	1803143	5368013
76-LL	18050	1762351	5249878	18049	1762351	5249869
76-LH	18535	1872620	5579700	18534	1872620	5579681
76-ML	16832	1696878	5055973	16831	1696878	5055962
76-MH	17278	1772882	5283077	17276	1772882	5283056
76-SL	15616	1621136	4831254	15615	1621136	4831240
76-SH	16049	1685680	5024009	16047	1685680	5023985
77A-LL	36565	160583	285420	36548	160582	285229
77A-LH	36631	160800	285803	36613	160800	285603

77A-ML	33590	147468	262108	33574	147468	261927
77A-MH	33674	147744	262594	33657	147743	262401
77A-SL	30612	134341	238773	30597	134341	238601
77A-SH	30716	134681	239373	30699	134680	239186
77B-LL	51115	160484	285245	51098	160484	285057
77B-LH	51250	160833	285861	51231	160833	285657
77B-ML	46953	147386	261962	46937	147385	261782
77B-MH	47105	147780	262657	47087	147779	262460
77B-SL	42798	134300	238701	42782	134300	238529
77B-SH	42954	134708	239420	42937	134708	239231
77C-LL	38375	160485	285246	38357	160484	285057
77C-LH	38487	160841	285875	38469	160841	285670
77C-ML	35261	147406	261997	35244	147405	261816
77C-MH	35378	147775	262649	35360	147775	262451
77C-SL	32141	134304	238708	32125	134304	238535
77C-SH	32274	134729	239457	32256	134728	239266
77D-LL	29490	160514	285297	29473	160513	285107
77D-LH	29593	160898	285975	29574	160898	285768
77D-ML	27105	147444	262065	27088	147444	261882
77D-MH	27212	147846	262774	27194	147846	262573
77D-SL	24712	134345	238780	24696	134345	238605
77D-SH	24824	134771	239532	24807	134771	239339
77E-LL	47133	160467	285215	47116	160467	285026
77E-LH	47242	160766	285742	47223	160766	285540
77E-ML	43298	147374	261941	43282	147374	261761
77E-MH	43418	147704	262523	43401	147704	262328
77E-SL	39457	134260	238631	39442	134260	238459
77E-SH	39590	134626	239275	39573	134626	239088
78A-LL	71798	160375	285052	71781	160375	284867
78A-LH	71921	160623	285489	71903	160622	285293
78A-ML	65930	147254	261728	65914	147253	261553
78A-MH	66081	147557	262264	66064	147557	262074
78A-SL	60072	134150	238436	60056	134150	238269
78A-SH	60248	134503	239059	60231	134503	238876

78B-LL	47677	160427	285145	47660	160427	284957
78B-LH	47759	160652	285542	47741	160652	285344
78B-ML	43792	147322	261850	43776	147322	261671
78B-MH	43893	147598	262337	43876	147598	262146
78B-SL	39905	134206	238535	39889	134206	238366
78B-SH	40022	134529	239105	40006	134529	238921
78C-LL	64975	160419	285130	64958	160419	284943
78C-LH	65099	160687	285603	65081	160687	285404
78C-ML	59673	147308	261825	59657	147308	261647
78C-MH	59821	147629	262391	59804	147629	262200
78C-SL	54370	134196	238516	54355	134195	238348
78C-SH	54536	134556	239153	54520	134556	238968
79-LL	33764	1301876	3824171	33762	1301876	3824149
79-LH	34379	1443213	4246742	34375	1443213	4246701
79-ML	31114	1239773	3644263	31112	1239773	3644240
79-MH	31710	1366147	4021990	31707	1366147	4021947
79-SL	28809	1201121	3533878	28806	1201121	3533852
79-SH	29333	1293779	3810627	29329	1293779	3810582
80A-LL	41857	67537	120004	41839	67537	119808
80A-LH	42013	67779	120432	41994	67779	120227
80A-ML	38537	62174	110471	38520	62173	110284
80A-MH	38728	62469	110994	38710	62469	110796
80A-SL	35559	57363	101923	35543	57363	101746
80A-SH	35805	57746	102598	35788	57745	102406
80B-LL	32839	66713	118539	32822	66713	118344
80B-LH	32925	66874	118822	32907	66873	118620
80B-ML	30221	61380	109061	30204	61380	108875
80B-MH	30340	61601	109451	30322	61601	109255
80B-SL	27885	56622	100605	27868	56622	100427
80B-SH	28032	56897	101090	28015	56897	100901
81A-LL	40068	160417	285126	40051	160417	284939
81A-LH	40154	160682	285594	40136	160682	285396
81A-ML	36809	147324	261852	36793	147323	261674
81A-MH	36910	147632	262395	36892	147631	262203

81A-SL	33548	134218	238555	33532	134217	238385
81A-SH	33666	134582	239197	33649	134581	239011
81B-LL	67650	160358	285023	67633	160358	284839
81B-LH	67792	160656	285548	67774	160656	285351
81B-ML	62134	147265	261749	62118	147265	261573
81B-MH	62301	147615	262366	62284	147615	262175
81B-SL	56611	134153	238442	56596	134153	238275
81B-SH	56795	134540	239124	56778	134540	238940
81C-LL	71229	160397	285092	71212	160397	284906
81C-LH	71438	160819	285835	71419	160818	285630
81C-ML	65433	147325	261855	65416	147325	261677
81C-MH	65648	147759	262620	65630	147759	262423
81C-SL	59621	134220	238560	59606	134220	238390
81C-SH	59845	134672	239357	59827	134672	239168
81D-LL	15756	161721	287428	15734	161721	287187
81D-LH	15860	162311	288470	15836	162311	288207
81D-ML	14515	148683	264250	14493	148682	264016
81D-MH	14607	149220	265199	14583	149219	264945
81D-SL	13267	135608	241009	13247	135608	240782
81D-SH	13348	136092	241865	13325	136092	241622
82A-LL	60101	160367	285038	60085	160367	284853
82A-LH	60192	160576	285406	60174	160575	285212
82A-ML	55195	147254	261729	55179	147254	261553
82A-MH	55310	147518	262195	55293	147518	262007
82A-SL	50285	134132	238403	50270	134131	238237
82A-SH	50431	134467	238995	50415	134467	238814
82B-LL	34829	67823	120512	34811	67823	120316
82B-LH	34944	68034	120886	34926	68034	120683
82B-ML	32090	62475	111008	32073	62475	110821
82B-MH	32243	62756	111504	32225	62756	111307
82B-SL	29614	57645	102423	29598	57644	102245
82B-SH	29810	58004	103057	29792	58003	102867
83A-LL	32081	66647	118423	32063	66647	118231
83A-LH	32209	66892	118854	32191	66891	118651

83A-ML	29530	61331	108975	29513	61331	108791
83A-MH	29676	61608	109463	29658	61608	109267
83A-SL	27255	56591	100551	27239	56591	100375
83A-SH	27429	56922	101133	27411	56921	100943
83B-LL	27500	66722	118554	27483	66721	118358
83B-LH	27502	66727	118563	27484	66727	118367
83B-ML	25302	61368	109040	25285	61368	108854
83B-MH	25334	61439	109166	25317	61439	108977
83B-SL	23332	56578	100526	23316	56577	100350
83B-SH	23409	56743	100818	23393	56743	100635
83C-LL	27947	66750	118604	27929	66750	118407
83C-LH	27928	66712	118537	27910	66712	118342
83C-ML	25708	61387	109073	25691	61387	108886
83C-MH	25726	61425	109140	25709	61425	108952
83C-SL	23702	56585	100539	23686	56585	100363
83C-SH	23764	56717	100772	23748	56716	100590
83D-LL	31318	66725	118559	31300	66725	118363
83D-LH	31272	66637	118405	31255	66637	118213
83D-ML	28809	61364	109032	28792	61364	108846
83D-MH	28779	61308	108934	28762	61308	108751
83D-SL	26555	56556	100488	26539	56555	100312
83D-SH	26569	56583	100536	26553	56583	100359
83E-LL	30983	66702	118519	30965	66701	118323
83E-LH	30975	66686	118492	30957	66686	118298
83E-ML	28508	61357	109020	28491	61357	108834
83E-MH	28521	61384	109068	28504	61384	108881
83E-SL	26280	56552	100482	26264	56552	100307
83E-SH	26351	56693	100729	26335	56692	100548
84A-LL	42963	67759	120398	42945	67759	120202
84A-LH	43301	68274	121308	43281	68274	121093
84A-ML	39582	62419	110907	39565	62419	110718
84A-MH	39928	62946	111837	39909	62945	111630
84A-SL	36560	57646	102425	36543	57646	102244
84A-SH	36907	58177	103362	36889	58176	103163

84B-LL	38706	67110	119241	38687	67110	119034
84B-LH	39062	67699	120281	39041	67699	120052
84B-ML	35681	61851	109893	35663	61851	109692
84B-MH	36015	62404	110871	35995	62404	110651
84B-SL	32974	57146	101531	32956	57145	101337
84B-SH	33280	57654	102430	33261	57654	102219
84C-LL	40305	66678	118478	40288	66678	118285
84C-LH	40507	66995	119037	40488	66995	118830
84C-ML	37110	61382	109065	37093	61382	108879
84C-MH	37327	61724	109668	37309	61724	109467
84C-SL	34243	56633	100625	34227	56633	100448
84C-SH	34484	57012	101293	34466	57012	101099
85-LL	42776	66872	118820	42758	66872	118621
85-LH	43112	67376	119710	43092	67376	119490
85-ML	39396	61579	109412	39378	61579	109221
85-MH	39729	62081	110298	39710	62081	110085
85-SL	36389	56872	101046	36373	56871	100861
85-SH	36692	57327	101851	36673	57327	101648
86A-LL	44383	66723	118556	44365	66722	118362
86A-LH	44656	67118	119254	44636	67118	119042
86A-ML	40854	61412	109117	40837	61412	108931
86A-MH	41152	61843	109878	41133	61843	109673
86A-SL	37706	56674	100697	37690	56674	100519
86A-SH	38007	57110	101467	37989	57110	101269
86B-LL	46200	67131	119277	46180	67131	119068
86B-LH	46605	67701	120283	46583	67701	120048
86B-ML	42580	61863	109913	42561	61862	109709
86B-MH	42979	62425	110906	42958	62425	110676
86B-SL	39342	57151	101539	39324	57151	101341
86B-SH	39734	57704	102514	39714	57704	102291
87A-LL	41440	67130	119276	41421	67130	119066
87A-LH	41861	67781	120423	41839	67780	120183
87A-ML	38177	61834	109862	38159	61834	109659
87A-MH	38604	62492	111022	38582	62491	110789

87A-SL	35311	57178	101586	35293	57177	101386
87A-SH	35688	57759	102611	35667	57759	102385
87B-LL	18524	29465	52305	18502	29464	52065
87B-LH	19318	30677	54443	19291	30676	54147
87B-ML	17291	27489	48794	17270	27489	48556
87B-MH	18074	28685	50903	18048	28685	50611
87B-SL	16056	25510	45276	16035	25510	45041
87B-SH	16736	26547	47105	16710	26547	46823

LL- large body weight, low lactation, LH- large body weight, high lactation, ML- moderate body weight, low lactation, MH- moderate body weight, high lactation, SL- small body weight, low lactation, SH- small body weight, high lactation

Table A.5

Estimates of total herd enteric methane production using a corn-based diet or a sorghum- based diet for each scenario (kilograms per year)

MLRA	Methane production for corn-based diets	Methane production for sorghum-based diets
102A-LL	9267	9368
102A-LH	9505	9611
102A-ML	8655	8751
102A-MH	8897	8998
102A-SL	8024	8116
102A-SH	8319	8416
102B-LL	9287	9382
102B-LH	9459	9558
102B-ML	8654	8745
102B-MH	8900	8996
102B-SL	8037	8124
102B-SH	8278	8369
102C-LL	9124	9228
102C-LH	9359	9468
102C-ML	8490	8590
102C-MH	8783	8888
102C-SL	7861	7956
102C-SH	8203	8304
106-LL	8278	8369
106-LH	8564	8660
106-ML	7869	7956
106-MH	8182	8275
106-SL	7432	7517
106-SH	7751	7841
112-LL	8054	8137
112-LH	8189	8275
112-ML	7683	7764
112-MH	7841	7926
112-SL	7287	7366
112-SH	7472	7555
116A-LL	9395	9430
116A-LH	9573	9609
116A-ML	8933	8966
116A-MH	9182	9218
116A-SL	8429	8461

116A-SH	8750	8785
116B-LL	9466	9501
116B-LH	9622	9658
116B-ML	8985	9019
116B-MH	9200	9235
116B-SL	8451	8484
116B-SH	8764	8798
117-LL	9366	9401
117-LH	9583	9619
117-ML	8885	8918
117-MH	9166	9202
117-SL	8389	8421
117-SH	8761	8795
118A-LL	9139	9172
118A-LH	9762	9799
118A-ML	8649	8681
118A-MH	9271	9307
118A-SL	8162	8193
118A-SH	8811	8846
118B-LL	8818	8848
118B-LH	9078	9109
118B-ML	8342	8371
118B-MH	8635	8666
118B-SL	7858	7886
118B-SH	8232	8262
119-LL	8215	8244
119-LH	9589	9625
119-ML	7909	7937
119-MH	9194	9229
119-SL	7694	7723
119-SH	8711	8745
133B-LL	8329	8363
133B-LH	9612	9654
133B-ML	7947	7980
133B-MH	9132	9172
133B-SL	7812	7845
133B-SH	8632	8670
135B-LL	8096	8126
135B-LH	9566	9603
135B-ML	7818	7848
135B-MH	9188	9225
135B-SL	7511	7540
135B-SH	8655	8690

150A-LL	9518	9544
150A-LH	9515	9543
150A-ML	8874	8899
150A-MH	9071	9097
150A-SL	8334	8358
150A-SH	8628	8654
150B-LL	8926	8954
150B-LH	9449	9480
150B-ML	8473	8500
150B-MH	9032	9062
150B-SL	8012	8039
150B-SH	8585	8615
152B-LL	8238	8269
152B-LH	9532	9571
152B-ML	7953	7984
152B-MH	9113	9150
152B-SL	7678	7708
152B-SH	8628	8664
42-LL	8568	8593
42-LH	9233	9261
42-ML	8266	8290
42-MH	8799	8825
42-SL	7843	7866
42-SH	8363	8388
53A-LL	10572	10572
53A-LH	10252	10252
53A-ML	9851	9851
53A-MH	9624	9624
53A-SL	9092	9092
53A-SH	8979	8979
53B-LL	9577	9577
53B-LH	10168	10168
53B-ML	9079	9079
53B-MH	9710	9710
53B-SL	8607	8607
53B-SH	9200	9200
53C-LL	9356	9356
53C-LH	9951	9951
53C-ML	8892	8892
53C-MH	9519	9519
53C-SL	8395	8395
53C-SH	9047	9047
54-LL	9164	9164

54-LH	9681	9681
54-ML	8571	8571
54-MH	9203	9203
54-SL	8112	8112
54-SH	8686	8686
55A-LL	9136	9235
55A-LH	9395	9498
55A-ML	8684	8780
55A-MH	8956	9057
55A-SL	8241	8334
55A-SH	8538	8636
55B-LL	9163	9275
55B-LH	9378	9494
55B-ML	8529	8635
55B-MH	8836	8947
55B-SL	7879	7979
55B-SH	8233	8339
55C-LL	8921	9015
55C-LH	9125	9224
55C-ML	8516	8608
55C-MH	8738	8834
55C-SL	8090	8179
55C-SH	8334	8428
56-LL	9547	9645
56-LH	9809	9913
56-ML	8880	8974
56-MH	9189	9289
56-SL	8225	8315
56-SH	8525	8621
58C-LL	8734	8734
58C-LH	9677	9677
58C-ML	8303	8303
58C-MH	9164	9164
58C-SL	7833	7833
58C-SH	8624	8624
58D-LL	8952	8952
58D-LH	9715	9715
58D-ML	8417	8417
58D-MH	9183	9183
58D-SL	7986	7986
58D-SH	8681	8681
60A-LL	8962	8962
60A-LH	9707	9707

60A-ML	8433	8433
60A-MH	9167	9167
60A-SL	7990	7990
60A-SH	8681	8681
61-LL	9392	9392
61-LH	9868	9868
61-ML	8814	8814
61-MH	9363	9363
61-SL	8226	8226
61-SH	8847	8847
62-LL	9196	9196
62-LH	9892	9892
62-ML	8636	8636
62-MH	9353	9353
62-SL	8161	8161
62-SH	8828	8828
63A-LL	8893	8893
63A-LH	9806	9806
63A-ML	8484	8484
63A-MH	9375	9375
63A-SL	8098	8098
63A-SH	8919	8919
63B-LL	9239	9239
63B-LH	9835	9835
63B-ML	8772	8772
63B-MH	9413	9413
63B-SL	8312	8312
63B-SH	8940	8940
64-LL	9202	9202
64-LH	9854	9854
64-ML	8676	8676
64-MH	9332	9332
64-SL	8143	8143
64-SH	8816	8816
65-LL	8712	8713
65-LH	9781	9784
65-ML	8379	8380
65-MH	9382	9385
65-SL	7915	7917
65-SH	8923	8926
66-LL	9006	9007
66-LH	9786	9789
66-ML	8512	8514

66-MH	9369	9372
66-SL	8137	8139
66-SH	8899	8902
67A-LL	8889	8890
67A-LH	9714	9716
67A-ML	8386	8388
67A-MH	9204	9207
67A-SL	7930	7932
67A-SH	8672	8675
70A-LL	8735	8759
70A-LH	9013	9038
70A-ML	8234	8257
70A-MH	8553	8578
70A-SL	7738	7760
70A-SH	8091	8114
70B-LL	8806	8829
70B-LH	9124	9150
70B-ML	8326	8348
70B-MH	8677	8702
70B-SL	7837	7859
70B-SH	8217	8241
71-LL	9008	9009
71-LH	9850	9852
71-ML	8566	8567
71-MH	9392	9394
71-SL	8148	8150
71-SH	8944	8947
72-LL	9257	9258
72-LH	9549	9551
72-ML	8746	8747
72-MH	9113	9115
72-SL	8258	8260
72-SH	8641	8643
73-LL	9091	9092
73-LH	9400	9401
73-ML	8556	8557
73-MH	8973	8975
73-SL	8111	8112
73-SH	8558	8560
74-LL	9359	9360
74-LH	9731	9733
74-ML	8854	8855
74-MH	9289	9291

74-SL	8421	8422
74-SH	8825	8828
75-LL	9117	9118
75-LH	9889	9891
75-ML	8658	8659
75-MH	9433	9435
75-SL	8240	8241
75-SH	8984	8987
76-LL	8564	8566
76-LH	9250	9252
76-ML	8179	8180
76-MH	8779	8781
76-SL	7795	7797
76-SH	8364	8367
77A-LL	9611	9634
77A-LH	9348	9373
77A-ML	8994	9016
77A-MH	8920	8943
77A-SL	8364	8385
77A-SH	8442	8464
77B-LL	9705	9728
77B-LH	9514	9539
77B-ML	9100	9122
77B-MH	9116	9140
77B-SL	8548	8569
77B-SH	8651	8674
77C-LL	9238	9261
77C-LH	9220	9244
77C-ML	8682	8704
77C-MH	8789	8813
77C-SL	8112	8133
77C-SH	8359	8382
77D-LL	8846	8869
77D-LH	9030	9055
77D-ML	8335	8357
77D-MH	8578	8602
77D-SL	7819	7840
77D-SH	8107	8131
77E-LL	9624	9647
77E-LH	9396	9420
77E-ML	9055	9077
77E-MH	8954	8977
77E-SL	8447	8467

77E-SH	8505	8528
78A-LL	10410	10432
78A-LH	9556	9580
78A-ML	9752	9773
78A-MH	9229	9252
78A-SL	9120	9140
78A-SH	8849	8871
78B-LL	9701	9724
78B-LH	9293	9317
78B-ML	9117	9138
78B-MH	8868	8891
78B-SL	8460	8481
78B-SH	8427	8449
78C-LL	10225	10247
78C-LH	9531	9555
78C-ML	9588	9609
78C-MH	9184	9207
78C-SL	8935	8955
78C-SH	8777	8799
79-LL	8312	8315
79-LH	9797	9802
79-ML	7949	7952
79-MH	9377	9382
79-SL	7804	7807
79-SH	8989	8994
80A-LL	10001	10025
80A-LH	9622	9646
80A-ML	9405	9427
80A-MH	9199	9223
80A-SL	8775	8796
80A-SH	8773	8796
80B-LL	9651	9675
80B-LH	9423	9447
80B-ML	9060	9082
80B-MH	8983	9007
80B-SL	8493	8515
80B-SH	8530	8553
81A-LL	9359	9382
81A-LH	9176	9201
81A-ML	8782	8804
81A-MH	8719	8742
81A-SL	8192	8212
81A-SH	8298	8320

81B-LL	10446	10468
81B-LH	9783	9807
81B-ML	9833	9854
81B-MH	9438	9461
81B-SL	9166	9186
81B-SH	9009	9031
81C-LL	10418	10440
81C-LH	9821	9846
81C-ML	9809	9831
81C-MH	9498	9522
81C-SL	9172	9192
81C-SH	9085	9108
81D-LL	8368	8397
81D-LH	9001	9033
81D-ML	8009	8038
81D-MH	8568	8598
81D-SL	7621	7649
81D-SH	8110	8140
82A-LL	10113	10135
82A-LH	9398	9422
82A-ML	9480	9502
82A-MH	9027	9049
82A-SL	8790	8810
82A-SH	8634	8656
82B-LL	9505	9529
82B-LH	9277	9302
82B-ML	8946	8969
82B-MH	8863	8886
82B-SL	8383	8404
82B-SH	8404	8427
83A-LL	9264	9287
83A-LH	9191	9216
83A-ML	8740	8763
83A-MH	8717	8741
83A-SL	8196	8217
83A-SH	8339	8362
83B-LL	9318	9342
83B-LH	9053	9077
83B-ML	8742	8765
83B-MH	8592	8615
83B-SL	8161	8183
83B-SH	8158	8180
83C-LL	9433	9457

83C-LH	9104	9128
83C-ML	8825	8848
83C-MH	8641	8664
83C-SL	8218	8240
83C-SH	8180	8202
83D-LL	9410	9434
83D-LH	9035	9058
83D-ML	8804	8826
83D-MH	8533	8555
83D-SL	8191	8213
83D-SH	8056	8078
83E-LL	9603	9627
83E-LH	9190	9213
83E-ML	9019	9042
83E-MH	8689	8711
83E-SL	8383	8404
83E-SH	8262	8284
84A-LL	9735	9758
84A-LH	9769	9795
84A-ML	9188	9211
84A-MH	9324	9350
84A-SL	8659	8681
84A-SH	8847	8872
84B-LL	9363	9388
84B-LH	9868	9895
84B-ML	8932	8956
84B-MH	9432	9459
84B-SL	8495	8518
84B-SH	8973	8998
84C-LL	9707	9731
84C-LH	9588	9613
84C-ML	9181	9204
84C-MH	9177	9202
84C-SL	8622	8643
84C-SH	8724	8748
85-LL	9570	9594
85-LH	9839	9866
85-ML	9065	9089
85-MH	9407	9433
85-SL	8600	8622
85-SH	8899	8923
86A-LL	9782	9806
86A-LH	9742	9768

86A-ML	9206	9228
86A-MH	9326	9350
86A-SL	8641	8663
86A-SH	8852	8876
86B-LL	9785	9810
86B-LH	9981	10009
86B-ML	9362	9387
86B-MH	9586	9614
86B-SL	8829	8853
86B-SH	9146	9173
87A-LL	9486	9511
87A-LH	9843	9872
87A-ML	8962	8986
87A-MH	9432	9460
87A-SL	8594	8618
87A-SH	8966	8994
87B-LL	8186	8215
87B-LH	9538	9573
87B-ML	7898	7927
87B-MH	9208	9244
87B-SL	7621	7649
87B-SH	8731	8765

LL- large body weight, low lactation, LH- large body weight, high lactation, ML- moderate body weight, low lactation, MH- moderate body weight, high lactation, SL- small body weight, low lactation, SH- small body weight, high lactation